



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143686

To: Ruixiang Li
Location: rem/4d75/4c70
Art Unit: 1646
Wednesday, February 02, 2005

Case Serial Number: 09/881736

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

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From: Li, Ruixiang
Sent: Sunday, January 30, 2005 2:41 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.09/881,736

Please do a standard search on:

SEQ ID NO: 2 against commercial amino acid databases.

QA-632

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

ME

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Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other CG

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:13:02 ; Search time 146 Seconds
(without alignments)
1563.938 Million cell updates/sec

Title: US-09-881-736a-2

Perfect score: 3243

Sequence: 1 MDTMILNVNLFPEQLVRRVE.....SKSATNIGROGNFFASPMLK 632

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: Published Applications_AA:*
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20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	9	US-09-881-736-2
2	3230	99.6	632	9	US-09-833-790-413
3	2919	90.0	570	9	US-09-833-790-427
4	2734	84.3	628	9	US-09-881-736-4
5	1182	36.4	255	16	US-10-408-765A-1045
6	541.5	16.7	681	9	US-09-881-736-6
7	334	10.3	2022	16	US-10-408-765A-598
8	322	9.9	175	15	US-10-072-012-878
9	310	9.6	1261	15	US-10-072-012-879
10	301	9.3	1261	14	US-10-177-980-2
11	301	9.3	1261	16	US-10-648-593-192
12	294.5	9.1	193	9	US-09-802-127-8
13					Sequence 8, Appl1

14	294	9.1	295	14	US-10-205-194-95	Sequence 95, Appl1
15	286.5	8.8	718	13	US-10-087-192-733	Sequence 733, App
16	286.5	8.8	1173	15	US-10-072-012-725	Sequence 725, App
17	286.5	8.8	1286	14	US-10-153-668-212	Sequence 212, App
18	286.5	8.8	1286	15	US-10-072-012-724	Sequence 724, App
19	286.5	8.8	1354	14	US-10-153-668-470	Sequence 470, App
20	286.5	8.8	1958	17	US-10-483-506-19	Sequence 19, Appl1
21	285.5	8.8	996	15	US-10-072-012-731	Sequence 731, App
22	285.5	8.8	1136	15	US-10-072-012-729	Sequence 729, App
23	285.5	8.8	1165	15	US-10-072-012-730	Sequence 730, App
24	285.5	8.8	1192	14	US-10-369-493-3502	Sequence 3502, Ap
25	284.5	8.8	1136	14	US-10-072-012-280	Sequence 280, App
26	284	8.8	1355	15	US-10-072-012-278	Sequence 278, App
27	275.5	8.5	1271	14	US-10-193-651-21	Sequence 21, Appl1
28	270.5	8.3	2548	9	US-09-851-682A-1	Sequence 1, Appl1
29	269.5	8.3	735	15	US-10-072-012-726	Sequence 726, App
30	269	8.3	615	13	US-10-087-192-736	Sequence 736, App
31	266.5	8.2	523	15	US-10-072-012-732	Sequence 732, App
32	263.5	8.1	555	9	US-09-764-868-878	Sequence 878, App
33	260.5	8.0	802	17	US-10-684-422-246	Sequence 246, App
34	258	8.0	903	16	US-10-408-765A-827	Sequence 827, App
35	256.5	7.9	659	16	US-10-363-829-303	Sequence 303, App
36	256.5	7.9	707	15	US-10-112-944-256	Sequence 256, App
37	255.5	7.9	1176	14	US-10-032-585-7782	Sequence 7782, Ap
38	255	7.9	589	14	US-10-094-749-1841	Sequence 1841, Ap
39	254.5	7.8	748	14	US-10-104-047-2336	Sequence 2336, Ap
40	253.5	7.8	1846	14	US-10-369-493-4974	Sequence 4974, Ap
41	251	7.7	170	9	US-09-802-127-7	Sequence 7, Appl1
42	251	7.7	170	13	US-10-080-960-32	Sequence 32, Appl1
43	247.5	7.6	291	9	US-09-764-868-898	Sequence 898, App
44	247.5	7.6	617	15	US-10-108-260A-4817	Sequence 4817, Ap
45	247	7.6	816	14	US-10-104-047-2328	Sequence 2328, Ap

ALIGNMENTS

RESULT 1
US-09-881-736-2
Sequence 2, Application US/09881736
Patent No. US20020076785A1
GENERAL INFORMATION:
APPLICANT: Glotzer, Michael
APPLICANT: Jantsch-Plunger, Verena
APPLICANT: Romano, Alper
APPLICANT: Mishima, Masanori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
FILE REFERENCE: 0652,2260001/EKS/AES
CURRENT APPLICATION NUMBER: US/09/881,736
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: EP 01 110 554.1
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/241,231
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: To be determined
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 632
TYPE: PRT
ORGANISM: Homo sapiens
US-09-881-736-2

Query Match 100.0%; Score 3243; DB 9; Length 632;
Best Local Similarity 100.0%; Pred No. 8.2e-258;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 ATERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQLIREMLMCDTSGSIQLSEB 120
Qy 121 QKSALAFNRGQSSSNAGNKRLLSTIDESGSIISDIPDKTDESLDWDSSLVKTFKLKR 180
      121 QKSALAFNRGQSSSNAGNKRLLSTIDESGSIISDIPDKTDESLDWDSSLVKTFKLKR
Db 121 QKSALAFNRGQSSSNAGNKRLLSTIDESGSIISDIPDKTDESLDWDSSLVKTFKLKR 180
Qy 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQGNESIVAKTIVVPNDGGPIEAVSTIETVP 240
      181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQGNESIVAKTIVVPNDGGPIEAVSTIETVP
Db 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQGNESIVAKTIVVPNDGGPIEAVSTIETVP 240
Qy 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGNGLHDFVSKTVIKPESC 300
      241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGNGLHDFVSKTVIKPESC
Db 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGNGLHDFVSKTVIKPESC 300
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      301 VPCGKRIRKFKLSLKCRDGRVVSHPBCRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB
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Qy 361 MIPSTIVHCVNIEQGLTETGLYRISGCDRTVKEKEKFLKVKTVPLLSKVDDIHAICS 420
      361 MIPSTIVHCVNIEQGLTETGLYRISGCDRTVKEKEKFLKVKTVPLLSKVDDIHAICS
Db 361 MIPSTIVHCVNIEQGLTETGLYRISGCDRTVKEKEKFLKVKTVPLLSKVDDIHAICS 420
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      421 LKDFLRNLKEPLLFRNLRAFMEAAEITDEDNSIAAMYQAVGELPOANRDTLAFIMIH
Db 421 LKDFLRNLKEPLLFRNLRAFMEAAEITDEDNSIAAMYQAVGELPOANRDTLAFIMIH 480
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Db 481 QVVAOSPHTKMDVANIARVFGPTIVAAVNPDPVTMSODIKRQKVERLLSLPLEYWS 540
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RESULT 2
US-09-833-790-413
; Sequence 413, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tonglong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 632
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-833-790-413

Query Match          99.6%; Score 3230; DB 9; Length 632;
Best Local Similarity 99.7%; Pred. No. 9,7e-257;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 121 QKSALAFNRGQSSSNAGNKRLLSTIDESGSIISDIPDKTDESLDWDSSLVKTFKLKR 180
Qy 181 EKRRSTSRQFVGPPEPVKKTSSIGSAVDQGNESIVAKTIVVPNDGGPIEAVSTIETVP 240
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Db 241 YWTRSRKKTGTIQLPNNSDSTLNSRQLEPRTETDSVGTPOSGNGLHDFVSKTVIKPESC 300
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      301 VPCGKRIRKFKLSLKCRDGRVVSHPBCRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB
Db 301 VPCGKRIRKFKLSLKCRDGRVVSHPBCRDRCPLPCIPILIGTPVKIGEGMLADFVSQTSB 360
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US-09-833-790-427
; Sequence 427, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tonglong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 570
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-833-790-427

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Best Local Similarity 99.8%; Pred. No. 3,4e-231;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 121 RSTSRQFVDPGPGPVKTRTSGISAVDOQNESIVAKTIVTVVPNDGGPIEAVSTIETVY 180
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Db 181 TRSRRTGTILQPNNSDTLNSRQLEBPTETDSVGTQPSNGMRLHDFVSKTVIKPES 240
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Db 301 PSIVHCVNEIEORGLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKVDIHAICSL 360
QY 423 KQFLRNKKEBLTLFRLNRAFMEAEITDEBNSIAAMYQAVGELPQANRDTLAFMLH 482
Db 361 KQFLRNKKEBLTLFRLNRAFMEAEITDEBNSIAAMYQAVGELPQANRDTLAFMLH 420
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Db 421 VQSPHTKMDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERLLSLLEYWSOF 480
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Db 481 MMEQENIDPLAHYIENSNAFSTPOTPDIKVSLGPTVTPHQLLTPSSSSLSQRYSTL 540
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Db 541 TKTTPRFSGSKSATNLGRQGNFPASPMLK 570

RESULT 4
US-09-881-736-4
; Sequence 4, Application US/09881736
; Patent No. US20020076785A1
; GENERAL INFORMATION:
; APPLICANT: Glotzer, Michael
; APPLICANT: Vantech-Plunger, Verena
; APPLICANT: Romano, Alper
; APPLICANT: Mishima, Masanori
; APPLICANT: Kaitna, Susanne
; TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their use in
; TITLE OF INVENTION: screening methods
; FILE REFERENCE: 0632,2260001/EKS/ABS
; CURRENT APPLICATION NUMBER: US/09/881,736
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: EP 00 112 880.0
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: EP 01 110 554.1
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/241,231
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: To be determined
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-881-736-4

Query Match 84.3%; Score 2734; DB 9; Length 628;
Best Local Similarity 84.4%; Pred. No. 6,7e-216;

Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3;
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Db 1 MOTMNLNENLFEQVLRVEILSEBNE-VQFIQLADPEDFRKKMORTHELCKYDILLM 60
QY 60 KAETRSALDVKLKHARNVDVEIKRORAEADCEKLEQOIQIRMLMCDTSGSIQISE 119
Db 61 KAETRSALDVKLKHARNVDVEIKRORAEADCEKLEQOIQIRMLMCDTSGSIQISE 120
QY 120 EOKSALAFINRGQSSSNAGNRLSTIDSGSLSDISPKTDESIDMDSLVKTKKREK 179
Db 121 EOKSALAFINRGQSSSNAGNRLSTIDSGSLSDISPKTDESIDMDSLVKTKKREK 180
QY 180 REKRSTSRQFVDPGPGPVKTRTSGISAVDOQNESIVAKTIVTVVPNDGGPIEAVSTIETVY 239
Db 181 REKRSTSRQFVDPGPGPVKTRTSGISAVDOQNESIVAKTIVTVVPNDGGPIEAVSTIETVY 240
QY 240 PYWTRSRRTGTILQPNNSDTLNSRQLEBPTETDSVGTQPSNGMRLHDFVSKTVIKPES 299
Db 241 PYWTRSRRTGTILQPNNSDTLNSRQLEBPTETDSVGTQPSNGMRLHDFVSKTVIKPES 300
QY 300 CVPCKGRIKFGKLSLKCRCRCRVVSHPECRCRCPCLPILIGTPVKIGEGMLADPFVSQTS 359
Db 301 CVPCKGRIKFGKLSLKCRCRCRVVSHPECRCRCPCLPILIGTPVKIGEGMLADPFVSQTS 360
QY 360 PMIPSIHCVNEIEORGLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKVDIHAIC 419
Db 361 PMIPSIHCVNEIEORGLTETGLYRISGCDRTVKELKEKFLKVKTVPLLSKVDIHAIC 420
QY 420 SLKQFLRNKKEBLTLFRLNRAFMEAEITDEBNSIAAMYQAVGELPQANRDTLAFMLH 479
Db 421 SLKQFLRNKKEBLTLFRLNRAFMEAEITDEBNSIAAMYQAVGELPQANRDTLAFMLH 480
QY 480 LQPVASQSPHTKMDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERLLSLLEYWSOF 539
Db 481 LQPVASQSPHTKMDVANLAVFPGTIVAHAVPNPDPTMODIKRQKVERLLSLLEYWSOF 540
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Db 541 SOPMMEQENIDPLAHYIENSNAFSTPOTPDIKVSLGPTVTPHQLLTPSSSSLSQRYSTL 596

RESULT 5
US-10-408-765A-1045
; Sequence 1045, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1045
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1045

Query Match 36.4%; Score 1182; DB 16; Length 255;

```

RESULT 6
US-09-881-736-6
Sequence 6, Application US/09881736
Patent No. US20020076785A1
GENERAL INFORMATION:
APPLICANT: Glotzer, Michael
APPLICANT: Jantsch-Plunger, Verena
APPLICANT: Romano, Alper
APPLICANT: Mishima, Masanori
APPLICANT: Kaitna, Susanne
TITLE OF INVENTION: Cyt-4 polypeptides, DNA molecules encoding them and their use in
TITLE OF INVENTION: screening methods
FILE REFERENCE: 0652.226001/EKS/AES
CURRENT FILING DATE: 2001-06-18
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: EP 00 112 880.0
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: EP 01 110 554.1
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/241,231
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: To be determined
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 681
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-881-736-6

```

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Db      247 CRDDGSGTPHOEMTTTTTTTTTTTTTTTTHNSAQNODPPRVSJLHQULRRBSLSCGSI PSCDQTP 3066
Qy      241 YWTRSRBKGTGLQPMWNSDSTLNSROLERPTETDSVGTPOSGNKRLLHDVPSKTVIKESG 3000
Db      307 GQTTNNIGLGMSSAILTKSTLDIRLTKGTAPMTNGTTR--DIARPHPIIEAGIKARKC 3653
Qy      301 VPGCKRIKFGKSLKCRDRCVVSHPECDRCPLPCIP-----TLIGTPVKGEGM 3566
Db      366 DKCATALYKLA--ISMKRDRCHQYVHHSSCCNKLHPETPRPKMTMTPKSALBRAXGAGEFR 4228
Qy      351 LADFVSQTSBMPISPIVHVCNEIEQRGLTETGLYRISGCDRTYKELKEKFLRYKTVPLLS 4100
Db      425 LQDLCTSAKRMIPAAVHCVALIEARGLTQEGIYAVPQGVRTYVNLDE--LRSKTVBNVG 4833
Qy      411 KVDIDHAGCSLKDPLRNKKEPULLFRLNRAFMEEAET--TDIEDNSTAATQAVGELPOA 4684
Db      484 -LHDVEVITDTLKRFLRDKDELIPRTSQEELIVANLYSTDPNGRLALNRVIELPOA 5422
Qy      469 NRDTLAFMLHIDLRV-AQSPHTKMDVANLAKYFGTIIYAAHVAPNDPVTMSQ-----D 5200
Db      543 NRDTLAVLFHIMKVIYAQSSRNKNKCEMAARVAPAVGHH-----PKVQSQSGALAGR 5966
Qy      521 IKQPKVERLLSLPEFYQSQFMWMEQENIDPLHYIENSNAFSTPQTPD-----IKVSLLG 5766
Db      597 ATDCHAMTALFEFDVYQWREFLGTSA-----VSMASNOIETARHODNFALCDRSILG 6494
Qy      577 PVUTPRHQLLKTPSSSSLSQVRSLTLKNTPRFGS 611
Db      650 PVTT-----SPATPLLRASNAVTRAGAAHLLGS 677

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RESULT 7
US-10-408-765A-598
; Sequence 598, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 598
; LENGTH: 2022
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-598

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Query Match	10.3%	Score 334	DB 16	Length 2022
Best Local Similarity	23.0%	Pred. No. 1.7e-17		
Matches 147	Conservative 111	Mismatches 266	Indels 116	Gaps 266
QY	22	LSEGNVEV-----FIOLADPFEDFRKQV---RTHELGLKXKDLMLKATERLSADV	70	
DB	1404	LSFSGSQVDSKSTFKRLFLKTKD-----KTKSLBEAELENAVSGHVLEATTMKKLEA	145	
QY	71	-----KLKHAENVDAEIKRQRAEADCEKLEIRQIOLIREMLCDTSGSIQLSEFOKALA	126	
DB	1459	PSGQGRHHAQE-----KRTKEPGGAKKKRNVRKI-----GKITVSEKMRSSVF	150	
QY	127	FLNRGGPSSSNAGNKRSLTIDE--SGSLLSDISFDKTESLMDWSLIVFTFLKKRERRS	165	
DB	1503	-----RQITNAN-----ELKTLDEFLINKINDLSQAKTP-----IESLFIETAEKFRS	154	
QY	186	TSRQFVDPGPGFPVKKTRISGSAVDQGNESIAKTTVTVPNDGCEIVANSTIER--VPYWR	244	


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Db      1546 NIKTMSVFNPKGI-----HVCYKDLMEVYQIVVSNLATERGQKDTNLVLNLFOSLIDEFTR 1601
Qy      245 SRRKTGLQPMWNSDSTLNSROLEPRTSDVGTVPQSGMRLLDHFVSKTYIKESGCVPGC 304
Db      1602 GYTK-----NPEFYKSKAQKKRKOERAVOENHG---HVFAYQVSIPOSCQCL 1650
Qy      305 KRIKFGKLSLKCRDCRVSHPECRDRCLPCLPPL--IGTP-VKIGE-GMLADFVSQTSF 360
Db      1651 SYIWMNDKALLGCVCKMTCHKKCVHKIQSHCSYTYGKSGPGAPGPHFGVCVDSLTSRKA 1710
Qy      361 MRSIVVHCNVEIQKGLTGTGLYRISGCRITYELKEKRLRYKTVPLSKVDD--IHAI 418
Db      1711 SVPIVTEKLEHEVMEGLYTEGLYRKSGAANRTRELFQ---ALQTPDAAYKLENFPHAI 1767
Qy      419 CSLIKDFLRNLYKEPLLTFRLNRAFMEEAITDENSIAMYOAVGELPOANRDTLAFMI 478
Db      1768 TGVKKQWLRLEPPLMTFPAQYGDPLRAVELPEKQOALATYAVLEHLPENAHNSLERLIF 1827
Qy      479 HLCQVA-QSPHTMDVANIKAKEFGPTIVAAHVPNDPVTMSODIKRQPKVVERLLSLPLE 537
Db      1828 HLKVALLEDVNMSPALALIFAPCLL-RCPNDSDELTKMKDYKLTTCVEMLIKQMR 1886
Qy      538 YMSQFMVVEQENIDPLHVIEN-----SNASTPTQTPD-----IKVSLIGPVT 579
Db      1887 KYK-----VKMEISIQLEAAESIAFRRLSLRQVANKSPKTRBPAGAGRLITTSRVSP-- 1940
Qy      580 TPEHOLKTPSSSSLSGRVST-----LTKTTPR 608
Db      1941 SPSTRNLALGSMRSALRTGTGRPARPGARALRRRPR 1980

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RESULT 8

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US-10-072-012-878
/ Sequence 878, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernhusen, Bryan
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Beha
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Molenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395

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/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 878
/ LENGTH: 175
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: GTPase-activator protein for Rho-like GTPases
US-10-072-012-878
Query Match 9.9%; Score 322; DB 15; Length 175;
Best Local Similarity 45.1%; Pred. No. 3.7e-18;
Matches 78; Conservative 25; Mismatches 64; Indels 6; Gaps 3;

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Qy      362 IRSIVVHCNVEIQKGLTGTGLYRISGCRITYELKEKRLRYKTVPLLSKVDIHIACSL 421
Db      3 IPIVKECTEYERKRLDTEGIRKSGASRYVELLEAPDSCGPDPLDSEYDVHVAQL 62
Qy      422 LKDFLNLKEPLLTFRLNRAFMEEAITDENSIAMYOAVGELPOANRDTLAFMIHQ 481
Db      63 LKFLFLEPEPLITFLFYEFTEIAKLEDEBERLRRLRELSLPPANRATLRYLLAHNL 122
Qy      482 RVAQ-SPHTRMDVANIKAKEFGPTIVAAHVPNDPVTMS-ODIKRQPKVVERLL 532
Db      123 RVAHSEBENKMTARNLAIVFGPTLR-----PPDGESASIKDIDHQNKVVEFLI 171

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RESULT 9

```

US-10-072-012-879
/ Sequence 879, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernhusen, Bryan
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Beha
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Molenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102

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Db 787 KMPNMCIEINRLLSKDLRLQIPASNFSIHLFVLHRLKRVVDHAEENKSNKGVLF 846
QY 501 GPTTAAVAVNPDPVTMSQ--DIKQPKYVERLLSLPLEYWSQFM---MVEQENIDPLH 554
Db 847 GBSLI-RPPTTAPITISSLAESYNQARLVFLIT-----YQKIDGSIQPDVWCISG 900
QY 555 VIENS--NAFSTPQTPDIKVSLLGPVTTPHQLKTPSSSSLSQVRSTLTNTPRFGS 611
Db 901 VDDGCFPKPLSPBERDIERSMKSLFFSSKEDIHTSESESKIFERAT5-----FEE 952
QY 612 KSKSATNLGR 621
Db 953 SERKQNALGK 962

RESULT 11
US-10-177-980-2
; Sequence 2, Application US/10177980
; Publication No. US20030166232A1
; GENERAL INFORMATION:
; APPLICANT: Saraa, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gomez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PAR6. A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PREPL
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177, 980
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/080, 855
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 08/805, 583
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-980-2

Query Match 9.3%; Score 301; DB 14; Length 1261;
Best Local Similarity 22.4%; Pred. No. 4.3e-15;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;
QY 9 RNIFEQLVRVVEILSGNEVQFIQAKDPEDPRKKWQRTDHE-LGKYKDLLMKAETERSA 67
Db 372 RLLEBALQKVE---EADELYKV-CVTNVEERRNDVENTKREILAQRLTLVFCDDTLKA 427
QY 68 LDVYKLGHANQVDEIKRRQRAADCEKLERQIQLIREMLMCTSGSIQISEQK---SA 124
Db 428 VTYNLFPHMQLQAASLADRLQSLCSGSAKLYDPGQEVSEFVKATNS-----TEBEKVDGAV 482
QY 125 LAFINRGQSSSNAGNKRLLSTI---DESGSILSDISFDKTDSELDWDSLVKTFKLKRE 181
Db 483 NKLHNSQPSGFGPANSLEADVRLPSSSKNIEEDRCNSADIT---GPSIRKWTGGMRS 539
QY 182 KRSTSRQFVDPGPVKKTRISIGSAVDQGNESIVAKTIVVPPNDGPIEAVSTIETVPY 241
Db 540 DEEST-----GSSSRSRLDS-----ESI-----SPGD----- 562
QY 242 WTRSRKKTGLQPMWNSDTLNSRQLEPRTT--DSVGTPOS---NGKRLHDFVSKTVIK 296
Db 563 FHKRLPRTSSGTMSSADDLDEREPSPSETGPNISLGTFRKTLMSKAALTHKF--RKLRS 620
QY 297 PESCVPCGRIKIFGKLSLKCRDGRVVSHEPCDRCP-PC---IP---TLIGTPVKIGRG 349
Db 621 PTKCRDCEGIVVF--QGVCECECLLVCHRKCLLENVILICGHQKLPKGIHLFG----- 670
QY 350 MLADF--VSQTSF-MIPSIIVHCVNEIBORGLTETGLYRISGCDRTVVKELKEKFLRVKTV 406

Db 671 --AEFTLVAKKBPDPFPLIKICASEIENRALCQGIYVCG-----NKIKTE 716
QY 407 PLTSKYD-----DI-----HAICSLKDFNLNKEPLTLFRNRAFWAEAB-----ITDB 451
Db 717 KICLALNEMHVLVDISEFSSHIDCVLKLYQLPPEPLFLFLYKXEFILAKELQVHNE 776
QY 452 DNS-----IAAMYQVGBLPOANDTALFMIHLQRYA-QSPHFK 490
Db 777 OETKNSLDEKMKPMNMCIEINRLLSKDLRLQIPASNFSIHLFVLHRLKRVVDHAEENK 836
QY 491 MOVANLAKYFEPPIVHANPNPD--PYTMSQ--DIKQPKYVERLLSLPLEYWSQFM--- 543
Db 837 MNSKNLGVIFGSPSLR--PRQTAPTITISSLAESYNQARLVFLIT-----YQKIDG 888
QY 544 -MVEQENIDPLHYENS--NAFSTPQTPDIKVSLLGPVTTPHQLKTPSSSSLSQVR 599
Db 889 SLQPDVWCISGIVDDGCFPKPLSPBERDIERSMKSLFFSSKEDIHTSESESKIFERAT 948
QY 600 STLTNTPRFGSKSKSATNLGR 621
Db 949 S-----FEESERKQNALGK 962

RESULT 12
US-10-648-593-192
; Sequence 192, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648, 593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406, 385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-192

Query Match 9.3%; Score 301; DB 16; Length 1261;
Best Local Similarity 22.4%; Pred. No. 4.3e-15;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;
QY 9 RNIFEQLVRVVEILSGNEVQFIQAKDPEDPRKKWQRTDHE-LGKYKDLLMKAETERSA 67
Db 372 RLLEBALQKVE---EADELYKV-CVTNVEERRNDVENTKREILAQRLTLVFCDDTLKA 427
QY 68 LDVYKLGHANQVDEIKRRQRAADCEKLERQIQLIREMLMCTSGSIQISEQK---SA 124
Db 428 VTYNLFPHMQLQAASLADRLQSLCSGSAKLYDPGQEVSEFVKATNS-----TEBEKVDGAV 482
QY 125 LAFINRGQSSSNAGNKRLLSTI---DESGSILSDISFDKTDSELDWDSLVKTFKLKRE 181
Db 483 NKLHNSQPSGFGPANSLEADVRLPSSSKNIEEDRCNSADIT---GPSIRKWTGGMRS 539
QY 182 KRSTSRQFVDPGPVKKTRISIGSAVDQGNESIVAKTIVVPPNDGPIEAVSTIETVPY 241
Db 540 DEEST-----GSSSRSRLDS-----ESI-----SPGD----- 562
QY 242 WTRSRKKTGLQPMWNSDTLNSRQLEPRTT--DSVGTPOS---NGKRLHDFVSKTVIK 296
Db 563 FHKRLPRTSSGTMSSADDLDEREPSPSETGPNISLGTFRKTLMSKAALTHKF--RKLRS 620
QY 297 PESCVPCGRIKIFGKLSLKCRDGRVVSHEPCDRCP-PC---IP---TLIGTPVKIGRG 349
Db 621 PTKCRDCEGIVVF--QGVCECECLLVCHRKCLLENVILICGHQKLPKGIHLFG----- 670

```

Oy 350 MLAD--VSOTP-NIPSVHCVNBIORGJTEGLTYISGCDRIVVKEKELFKV 406
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 671 --AETTVAKKEPDGIFILIKCASIEHNRALCLOIYVCG-----NKITE 716
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 407 PLSKVD-----DI-----HAISLLKPLRNKKEPLTFRINRAEMAE---ITDE 451
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 717 KLCLALENGMLVLDISESSHDI CDVLKYLKRLPFPFLFRLYKEFIDLAKIIOHNEE 766
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 452 DNS-----IAMYOAVGSLPOANRDTLFLNIIHLORVA--OSPHTK 490
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 777 QETKNLSLEDKKPMNMCIEINRILILSKSOLNQLPASNNNSLHFLVHLKRVVDHAEK 836
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 491 MDVANLAKVFGCTTYAHAVNPD--PYTMSQ--DIRQPKVVERLLSLPLEYNSQEM--- 543
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 837 MNSKRLGVIFGSLIR--PRPQTAITITISLAEYNSQARLVEFLT-----VSQKIFDG 888
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 544 -MVEQENIDPLHVIENS--NAFSTPQTPDIKSLILGPATTPPEHOLIKTPSSSSLSQVR 599
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 889 SLQPDVWCISIVVQCGCFPKPLLSPEHRDIESMKSMLPSSSEDIDHTSESEKITERAT 948
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 600 SLTKNTRPFGSKSKSATNUGR 621
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 949 S-----FEESERQNALGK 962
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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```

RESULT 13
US-09-802-127-8
/ Sequence 8, Application US/09802127
/ Patent No. US20020045212A1
/ GENERAL INFORMATION:
/ APPLICANT: Glucksmann, Maria Alexandra
/ APPLICANT: Meyers, Rachel
/ TITLE OF INVENTION: No. US20020045212A1e1 Human GTPase Activator Proteins
/ FILE REFERENCE: 035800/158999
/ CURRENT FILING DATE: US/09/802,127
/ PRIOR APPLICATION NUMBER: 2001-02-23
/ PRIOR FILING DATE: 2000-02-29
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 193
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Rho-Gap3 consensus sequence
US-09-802-127-8

```

Query Match	9.1%	Score 294.5	DB 9	Length 193
Best Local Similarity	40.1%	Pred. No. 86-16	Indels 41	Gaps 8
Matches	81	Conservative	26	Mismatches 54
Qy	359	SPMIPSIIVHCVNIEBORGITETGTYLRISGCDRTYKELKEKFLRYKVPYPLSKVD----	413	
Db	1	SP-IPITVEKCTEYLEKRGCLDTREGIYRVSQSKRYVELREAPDGSDD--LDSLSDEITE	57	
Qy	414	-----DIHACGLKDFLNKLEPPLTFPLNAPFMAAII-----TDE	451	
Db	58	ESEDIEEYDVHVAAGLKLKYLELEPPLTFELYEEFLEAAKLYQIEATSRROSEKSEDE	117	
Qy	452	DNISIAMYQAVGSELQOANRDTLAFMIHLQRYAQ--SPHKMDVANAIAKVFGEPTIVAAVP	510	
Db	118	EERLEALNELLSLPPANRATIRYL-LHNRRVAEHSVVKMTARNLAIVFGFTLLR----	172	
Qy	511	NDDPYTMSODIKRQKPVVERLL	532	
Db	173	--PPLT--DIKGNKVVETLL	189	

RESULT 14
US-10-205-194-95
; Sequence 95, Application US/10205194
; Publication No. US20030134301A1

```

: GENERAL INFORMATION:
: APPLICANT: Warner-Lambert Company
: APPLICANT: Lee, Kevin
: APPLICANT: Dixon, Alistair
: APPLICANT: Brooksbank, Robert
: APPLICANT: Plimock, Robert
: TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
: FILE REFERENCE: WL-A-018201
: CURRENT APPLICATION NUMBER: US/10/205,194
: CURRENT FILING DATE: 5200-07-24
: PRIOR APPLICATION NUMBER: GB 0118354.0
: PRIOR FILING DATE: 2001-07-27
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 95
: LENGTH: 295
: TYPE: PRT
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Beta chimerin
: US-10-205-194-95

```

	Query Match	9.1%	Score 294;	DB 14;	Length 295;
	Best Local Similarity	29.3%	Pred. No. 1,7e-15;		
	Matches	81;	Conservative	52;	Mismatches 111; Indels 33; Gaps 8
Oy					
Db	285 RLHDFVSKTVIKPESCPGKKRIKFGKLS--LKCDRCRVSHPEBCRDRCPLPCIPPLIST	342			
	: :: :	:			
Db	40 KTHNFKVTPTFRPGPHNCYCA-NFMWGLTAOGRCCDGLNVHKQSKHVNPNDOPDLKRI	98			
Oy	343 PVKIIGEGMLADPVQSOTSPMISIVAHCVNEIEFORGLTGTGLRISGCDTEVELKEFLR	402			
Db	99 K-KYYCCDLTLVKAHNTORFPMVVDICIRREIARLKBEGLYRGSGFTIHIDVKAFFR	157			
Oy	403 VKTVPLLSKVd-----DIHAISCLDKDFLNKEPLLTFPLNFAMFAALITDEDSNI	455			
Db	158 DG-----EKAISANIYPDININITALKLYEPFDLPILPIITYDTYKFIEAAATISNDEBL	212			
Oy	456 AAMYQAVGELPOANDDTLAFLMIHLHORVAOSPHTK-MOVANLAKYGFPTIVAHAVENDDP	514			
Db	213 EAVHEVLMLLPRAHETIETRLIMIHIAKTYMANEKXLMNAENNGIYFGPIILM--RPEDSST	270			
Oy	515 VTMSODIRKPQVERLLSLPLEYWSQPMMAEQENI	550			
Db	271 LTTLDNRKYOKLIYO-----ILLENEDEV	293			

```

RESULT 15
US-10-087-192-333
; Sequence 333, Application US/10087192
; Publication NO. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
;
; LENGTH: 718
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-333

```

Query Match	8.8%;	Score 286.5;	DB 13;	Length 718,
Best Local Similarity	23.8%;	Pred. No. 2.8e-14;		

Matches 154; Conservative 111; Mismatches 258; Indels 125; Gaps 25;

[illegible]

Search completed: February 1, 2005, 14:23:09
Job time : 148 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 13:56:16 : Search time 164 Seconds
(without alignments)
1382.420 Million cell updates/sec

Title: US-09-881-736A-2

Perfect score: 3243
Sequence: 1 MDTMMLNVLNFEQLVRVE.....SKSATNLGRQNFASPMLEK 632

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3237	99.8	632	4	ABU53065
2	3237	99.8	632	7	ADE60209
3	3237	99.8	632	7	ADPE5165
4	3237	99.8	632	8	ADO20214
5	3233	99.7	632	4	AAM40047
6	3230	99.6	632	5	AAM69419
7	2919	90.0	570	5	AU69422
8	2734	84.3	628	7	ADE60207
9	1182	36.4	255	4	AAB94223
10	1182	36.4	255	7	ADU59239
11	971.5	30.0	256	4	AU32069
12	864	26.6	625	4	ABB68056
13	625	19.3	4318	4	ABG14787
14	618	19.1	1086	4	ABG10230
15	618	19.1	1086	4	ABG10230
16	618	19.1	1086	4	ABG13958
17	581	17.9	119	4	AAM41833
18	477	14.7	384	4	ABBS9247
19	334	10.3	2022	6	ADJ68792
20	323.5	10.0	1240	6	ABR41659
21	323.5	10.0	2158	7	ADD18702
22	322	9.9	175	5	AD117343
23	322	9.9	175	5	AD117342
24	322	9.9	334	4	AAM39659
25	322	9.9	352	4	AAM41445

26	322	9.9	476	6	ABR41263	ABR41263 Human DIT
27	310	9.6	1261	5	AD117197	AD117197 Human NOV
28	301	9.3	1261	5	AAW75995	AAW75995 GRPase ac
29	301	9.3	1261	3	AAV90268	AAV90268 Human GTP
30	301	9.3	1261	8	ADL61268	ADL61268 Human TYR
31	294.5	9.1	193	4	AA667553	AA667553 Amino acyl
32	294	9.1	295	7	ADB85214	ADB85214 Rat chima
33	294	9.1	1019	6	ADAI3329	ADAI3329 Human int
34	293.5	9.1	466	6	ABR58660	ABR58660 Human can
35	293.5	9.1	468	7	ADBS9897	ADBS9897 Human pro
36	290.5	9.0	736	2	AAW7809	AAW7809 Human GTP
37	290.5	9.0	759	4	ABG16793	ABG16793 Novel hum
38	290.5	9.0	800	4	ABG16794	ABG16794 Novel hum
39	290.5	9.0	926	7	ADG90731	ADG90731 Hepatic s
40	286.5	8.8	856	3	AA841660	AA841660 Human ORF
41	286.5	8.8	1173	4	AA897911	AA897911 Human G-P
42	286.5	8.8	1173	5	AD117189	AD117189 Human NOV
43	286.5	8.8	1286	5	AD117188	AD117188 Human NOV
44	286.5	8.8	1286	7	ADG10622	ADG10622 Human STA
45	286.5	8.8	1354	7	ADG10880	ADG10880 Human STA

ALIGNMENTS

RESULT 1
ID ABU53065 standard; protein; 632 AA.
XX ABU53065;
AC
XX
DT 14-APR-2003 (first entry)
XX
DE Human signal transduction-associated protein from DKFZphtes3_1c1.
XX
KW Human; gene therapy; vaccine; disease treatment; detection.
XX
OS Homo sapiens.
XX
PN W0200112659-A2.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-IB001496.
XX
PR 18-AUG-1999; 99US-0149499P.
XX
PR 28-SEP-1999; 99US-0156503P.
XX
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
XX
N-PSDB; ABX71357.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies.
XX
PS Claim 21; Page 659; 1095pp; English.
XX
CC This invention describes novel polynucleotides and polypeptides isolated
XX from human cDNA libraries which can be used for gene therapy or in
XX vaccines. The polynucleotides can be used for the prevention and treatment of diseases
XX associated with inappropriate polypeptide expression. The products of the
XX invention may also be used to identify modulators of expression and
XX activity and to down regulate expression and activity. The antibodies of
XX the invention may also be used as diagnostic agents for detecting the
XX presence of polypeptides in samples. This sequence represents a
XX polypeptide described in the disclosure of the invention
XX
XX Sequence 632 AA;

Query Match 99.8%; Score 3237; DB 4; Length 632;
Best Local Similarity 99.8%; Pred. No. 2.2e-263;
Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTMMLNVNRLFEQVLRRVEIISSENEVOFIQLADFEPRKKMORTDHELGYKDLMLK 60
DB 1 MDTMMLNVNRLFEQVLRRVEIISSENEVOFIQLADFEPRKKMORTDHELGYKDLMLK 60
QY 61 AETERSALDVKLKHANQVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQLSBE 120
DB 61 AETERSALDVKLKHANQVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQLSBE 120
QY 121 QKSALAFLNRGQPSSSNAGNKRSLSTIDSGSILSDISFPKTBESLDWDSLVKTFKLKR 180
DB 121 QKSALAFLNRGQPSSSNAGNKRSLSTIDSGSILSDISFPKTBESLDWDSLVKTFKLKR 180
QY 181 EKRRSTSRQFVDGPPVPVKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
DB 181 EKRRSTSRQFVDGPPVPVKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
QY 241 YWTRSRRTKGTIQLPWNDSSTLNSRQLEPRTETDSVGTPOSGMRLLHDFVSKTVIKPESC 300
DB 241 YWTRSRRTKGTIQLPWNDSSTLNSRQLEPRTETDSVGTPOSGMRLLHDFVSKTVIKPESC 300
QY 301 VPCGKRIRFGKSLKCRDQVSVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSBP 360
DB 301 VPCGKRIRFGKSLKCRDQVSVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSBP 360
QY 361 MIPSIIVHCVNEIEQGLTETGTYRISGCDRTYKELKEKFLRVKTVPLLSKVDIDHAFIS 420
DB 361 MIPSIIVHCVNEIEQGLTETGTYRISGCDRTYKELKEKFLRVKTVPLLSKVDIDHAFIS 420
QY 421 LKQDFLRNLKEPLLTERLNRAFMEEAEITDEDSISIAMTQAVGELPQANRDTLAFIMIH 480
DB 421 LKQDFLRNLKEPLLTERLNRAFMEEAEITDEDSISIAMTQAVGELPQANRDTLAFIMIH 480
QY 481 QKVAOSPHTRKMVYANLAKVFGPTVAHAVPNPVTMSQDIKQKQVVERLLSPLEFYS 540
DB 481 QKVAOSPHTRKMVYANLAKVFGPTVAHAVPNPVTMLDIDKQKQVVERLLSPLEFYS 540
QY 541 QPMVAVQENIDPLHVIENSNAFSTPQTPDIKVSLGPVTPPHQLKTPSSSSLSQRVSS 600
DB 541 QPMVAVQENIDPLHVIENSNAFSTPQTPDIKVSLGPVTPPHQLKTPSSSSLSQRVSS 600
QY 601 TLTNTPRFGSKSKSATNLGRQGNFPASPMLK 632
DB 601 TLTNTPRFGSKSKSATNLGRQGNFPASPMLK 632

RESULT 2
ADE60209
ID ADE60209 standard; protein; 632 AA.
XX
AC ADE60209;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein CAB66728, SEQ ID NO 6115.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN MO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-033347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; CAB66728.
PT New composition comprising two or more isolated polypeptides, useful for
PS preparing a medicament for treating pain in an animal.
PS Claim 1; Page; 1017p; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPRO at
CC ftp.wipro.int/pub/published_pct_sequences.
XX
SQ Sequence 632 AA;

Query Match 99.8%; Score 3237; DB 7; Length 632;
Best Local Similarity 99.8%; Pred. No. 2.2e-263;
Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTMMLNVNRLFEQVLRRVEIISSENEVOFIQLADFEPRKKMORTDHELGYKDLMLK 60
DB 1 MDTMMLNVNRLFEQVLRRVEIISSENEVOFIQLADFEPRKKMORTDHELGYKDLMLK 60
QY 61 AETERSALDVKLKHANQVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQLSBE 120
DB 61 AETERSALDVKLKHANQVDVEIKRORAEADCEKLEROIQLIREMLMCDTSGSIQLSBE 120
QY 121 QKSALAFLNRGQPSSSNAGNKRSLSTIDSGSILSDISFPKTBESLDWDSLVKTFKLKR 180
DB 121 QKSALAFLNRGQPSSSNAGNKRSLSTIDSGSILSDISFPKTBESLDWDSLVKTFKLKR 180
QY 181 EKRRSTSRQFVDGPPVPVKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
DB 181 EKRRSTSRQFVDGPPVPVKTRISGSAVDQGNESIAKTTVVPNDGPIEAVSTIETVP 240
QY 241 YWTRSRRTKGTIQLPWNDSSTLNSRQLEPRTETDSVGTPOSGMRLLHDFVSKTVIKPESC 300
DB 241 YWTRSRRTKGTIQLPWNDSSTLNSRQLEPRTETDSVGTPOSGMRLLHDFVSKTVIKPESC 300
QY 301 VPCGKRIRFGKSLKCRDQVSVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSBP 360
DB 301 VPCGKRIRFGKSLKCRDQVSVSHPECRCRCPICPTLIGTPVKIGEGMLADFVSQTSBP 360

QY 361 MIPSIYVHCNVEIEORGLTETGLYRISGCRTRYKELKEKPLRYKTVPLLSKVDIAHICS 420
 DB 361 MIPSIYVHCNVEIEORGLTETGLYRISGCRTRYKELKEKPLRYKTVPLLSKVDIAHICS 420
 QY 421 LKDPFLNLKEPLTLFRLNAPFMEAAITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 DB 421 LKDPFLNLKEPLTLFRLNAPFMEAAITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 QY 481 QRAVASPHTMDVANIYAKVGPRTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 DB 481 QRAVASPHTMDVANIYAKVGPRTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 QY 541 QFMMVBOENIDPLHVIENSNAFSTPQTPDIKVSILGVPVTPHQLKTPSSSSLSQYRS 600
 DB 541 QFMMVBOENIDPLHVIENSNAFSTPQTPDIKVSILGVPVTPHQLKTPSSSSLSQYRS 600
 QY 601 TLTKNTPRFGSKSKSATNLGRQGNFASPMLK 632
 DB 601 TLTKNTPRFGSKSKSATNLGRQGNFASPMLK 632

RESULT 3

ID ADP65165 standard; protein; 632 AA.
 XX ADP65165;
 AC
 XX
 DT 12-AUG-2004 (first entry)
 XX

Human Rac GTPase activating protein 1, GTPase activating protein.

XX autoimmune disease; arthritis; gene expression analysis;
 XX rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KM antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KM immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KM fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KM immune; human.

XX Homo sapiens.

XX MO2003072827-A1.

XX 04-SEP-2003.

XX 31-OCT-2002; 2002MO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thornton SL;

XX WPI, 2003-712740/67.

XX GENBANK: NP_037409.

XX Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

XX Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

XX SO Sequence 632 AA;

Query Match 99.8%; Score 3237; DB 7; Length 632;
 Best Local Similarity 99.8%; Pred. No. 2.2e-263;
 Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDTMMLNVRLLFEOLVRRVILLSEGNVOTIOLAKDPEDRRKKMQRDHELKTKDILMK 60
 DB 1 MDTMMLNVRLLFEOLVRRVILLSEGNVOTIOLAKDPEDRRKKMQRDHELKTKDILMK 60
 QY 61 AETERSALDVKLGKARQVVEIKRORADCEKLERQIOLIREMLMCTSGSIQJSEE 120
 DB 61 AETERSALDVKLGKARQVVEIKRORADCEKLERQIOLIREMLMCTSGSIQJSEE 120
 QY 121 OKSALAFNLNGQSSSSNAGKRLSTIDSGSILSDISFDXTDESLDWDSSLVTKFKLKR 180
 DB 121 OKSALAFNLNGQSSSSNAGKRLSTIDSGSILSDISFDXTDESLDWDSSLVTKFKLKR 180
 QY 181 EKRRSTSRQVNDPPGVKTRISGANVQGNISYAKTVTVPNQGGPIEAUSTETVP 240
 DB 181 EKRRSTSRQVNDPPGVKTRISGANVQGNISYAKTVTVPNQGGPIEAUSTETVP 240
 QY 241 YMTRSRRTGTLQPMNSDSTLNSRQLEPRRETSGVGTPOSGGKRLHDFVSKTVIKPESC 300
 DB 241 YMTRSRRTGTLQPMNSDSTLNSRQLEPRRETSGVGTPOSGGKRLHDFVSKTVIKPESC 300
 QY 301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDCPLPCIPITLLIGTPVKIGEGMLADFVSGTSP 360
 DB 301 VPCGKRIKFGKLSLKCRDCRVVSHPECRDCPLPCIPITLLIGTPVKIGEGMLADFVSGTSP 360
 QY 361 MIPSIYVHCNVEIEORGLTETGLYRISGCRTRYKELKEKPLRYKTVPLLSKVDIAHICS 420
 DB 361 MIPSIYVHCNVEIEORGLTETGLYRISGCRTRYKELKEKPLRYKTVPLLSKVDIAHICS 420
 QY 421 LKDPFLNLKEPLTLFRLNAPFMEAAITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 DB 421 LKDPFLNLKEPLTLFRLNAPFMEAAITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 QY 481 QRAVASPHTMDVANIYAKVGPRTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 DB 481 QRAVASPHTMDVANIYAKVGPRTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
 QY 541 QFMMVBOENIDPLHVIENSNAFSTPQTPDIKVSILGVPVTPHQLKTPSSSSLSQYRS 600
 DB 541 QFMMVBOENIDPLHVIENSNAFSTPQTPDIKVSILGVPVTPHQLKTPSSSSLSQYRS 600
 QY 601 TLTKNTPRFGSKSKSATNLGRQGNFASPMLK 632
 DB 601 TLTKNTPRFGSKSKSATNLGRQGNFASPMLK 632

RESULT 4

AD020214
 ID AD020214 standard; protein; 632 AA.

XX AD020214;
 AC
 XX
 XX

DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #559.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI: 2004-420667/39.
 DR N-PSDB; ADO20213.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7, SEQ ID NO 1118, 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 CC
 SQ Sequence 632 AA;
 Query Match 99.8%; Score 3237; DB 8; Length 632;
 Best Local Similarity 99.8%; Pred. No. 2,2e-263;
 Matches 631; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDTMNLVNLVFEQVLRVVEILSEGNVQFIQLAKDFEPRKKKQRTDHLGKYKDLNKK 60
 DB 1 MDTMNLVNLVFEQVLRVVEILSEGNVQFIQLAKDFEPRKKKQRTDHLGKYKDLNKK 60
 QY 61 AETERSALDVKLGHANQVDEIKRRQRAADCEKLEROIQLIREMLMCDTSGSIQLSEE 120
 DB 61 AETERSALDVKLGHANQVDEIKRRQRAADCEKLEROIQLIREMLMCDTSGSIQLSEE 120
 QY 121 QKSALAFNRGQSSNNAQNKRLSTIDSGSIIISDTSFPTKDSLWDSLVVTFKLKKR 180
 DB 121 QKSALAFNRGQSSNNAQNKRLSTIDSGSIIISDTSFPTKDSLWDSLVVTFKLKKR 180
 QY 181 EKRRSTSRQFVDPGPPVKKTRISGSAVQGNESIAKTTVTVPNDGCPLEAVSTLETVP 240
 DB 181 EKRRSTSRQFVDPGPPVKKTRISGSAVQGNESIAKTTVTVPNDGCPLEAVSTLETVP 240

QY 241 YWTRSRRTKGTI QPMNSDSTLNSRQLERTETDVSIGTQSGNGLHDPVSKTVIKPESC 300
 DB 241 YWTRSRRTKGTI QPMNSDSTLNSRQLERTETDVSIGTQSGNGLHDPVSKTVIKPESC 300
 QY 301 VPCGRIRKFKGSLKCRDPRVVSHEPCDRCPICPILTIGTPVYKIGEMLADPVSQTSF 360
 DB 301 VPCGRIRKFKGSLKCRDPRVVSHEPCDRCPICPILTIGTPVYKIGEMLADPVSQTSF 360
 QY 361 MIPSIIVHGVNEIEORGLTETGLYRISGCDRTVKEIKFKFLKVKTVPLLSKYVDIHAIQS 420
 DB 361 MIPSIIVHGVNEIEORGLTETGLYRISGCDRTVKEIKFKFLKVKTVPLLSKYVDIHAIQS 420
 QY 421 LKDFLRNKEPFLFLFRNARMEAAETDENSTIAAMYQAVGELPQANRDTLAFMLHL 480
 DB 421 LKDFLRNKEPFLFLFRNARMEAAETDENSTIAAMYQAVGELPQANRDTLAFMLHL 480
 QY 481 QRAVSPHTKMDVANAIAKVFPTIYAAHVAPNDPVTMSODIKRQKVERLSTPLEYWS 540
 DB 481 QRAVSPHTKMDVANAIAKVFPTIYAAHVAPNDPVTMLQDIKQKVERLSTPLEYWS 540
 QY 541 QFMVVEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPBHLLKTPSSSSLSQRYVS 600
 DB 541 QFMVVEQENIDPLAVIENSNAFSTPQTPDIKVSLLGPVTPPBHLLKTPSSSSLSQRYVS 600
 QY 601 TLTNTPTPRFGSKSKSATNLGROGNFPAGPMLK 632
 DB 601 TLTNTPTPRFGSKSKSATNLGROGNFPAGPMLK 632
 XX
 RESULT 5
 ID AAM40047
 ID AAM40047 standard; protein; 632 AA.
 AC AAM40047;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 3192.
 XX
 KW Human; nocrotic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00652191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Dimaenac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB; AA159203.
 XX

PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

PS Example 4; SEQ ID NO 3192; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (AA438642-AA442213) with nucleotide.
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activation/inhibition activity, chemocytic/chemokinetic activity, haemostatic
 CC and thrombotic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 632 AA:

Query Match 99.7%; Score 3233; DB 4; Length 632;
 Best Local Similarity 99.7%; Pred. No. 4.8e-263;
 Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MDTMMLNVNRLFEQVLRVVEILSEGNEVOFIQAKDFEDRRKKMQRTDHELGYKQDLMK 60
 1 MDTMMLNVNRLFEQVLRVVEILSEGNEVOFIQAKDFEDRRKKMQRTDHELGYKQDLMK 60
 61 AETERBALDVKLKHAANQVDVEIKRQRAADCEKLEKEROIQLIREMLMCDTSSIQLSSE 120
 61 AETERBALDVKLKHAANQVDVEIKRQRAADCEKLEKEROIQLIREMLMCDTSSIQLSSE 120
 121 QXSALAFPLNRGQSSSNAGNKLSTIDESGSIISDISFDKTDESLDWDSSLVKTFKLR 180
 121 QXSALAFPLNRGQSSSNAGNKLSTIDESGSIISDISFDKTDESLDWDSSLVKTFKLR 180
 121 QXSALAFPLNRGQSSSNAGNKLSTIDESGSIISDISFDKTDESLDWDSSLVKTFKLR 180
 121 QXSALAFPLNRGQSSSNAGNKLSTIDESGSIISDISFDKTDESLDWDSSLVKTFKLR 180
 181 EKRRSRSTROFVDPGPPGVKTRISIGSAVNDGNSIYAKTVVNNCGPIEAISTETVP 240
 181 EKRRSRSTROFVDPGPPGVKTRISIGSAVNDGNSIYAKTVVNNCGPIEAISTETVP 240
 181 EKRRSRSTROFVDPGPPGVKTRISIGSAVNDGNSIYAKTVVNNCGPIEAISTETVP 240
 241 YWTRSRKKTGTLQPMNSDSTLNSROLEPRTEQSVGTPOSGNGRLHDFVSKTVIKPESC 300
 241 YWTRSRKKTGTLQPMNSDSTLNSROLEPRTEQSVGTPOSGNGRLHDFVSKTVIKPESC 300
 241 YWTRSRKKTGTLQPMNSDSTLNSROLEPRTEQSVGTPOSGNGRLHDFVSKTVIKPESC 300
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRDCPLPCIPETLIGTPVKIGEGMLADPVSGTSP 360
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRDCPLPCIPETLIGTPVKIGEGMLADPVSGTSP 360
 301 VPCGKRIKFGKLSLKCRCDCRVVSHPECRDCPLPCIPETLIGTPVKIGEGMLADPVSGTSP 360
 361 MIPSIYVHCNLEIEQGLTETGTYRISGCRVYKELKELKRLRYKTVPLSKVDIHAICS 420
 361 MIPSIYVHCNLEIEQGLTETGTYRISGCRVYKELKELKRLRYKTVPLSKVDIHAICS 420
 361 MIPSIYVHCNLEIEQGLTETGTYRISGCRVYKELKELKRLRYKTVPLSKVDIHAICS 420
 421 LKQDFRLNKEPLTLFRLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 421 LKQDFRLNKEPLTLFRLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 421 LKQDFRLNKEPLTLFRLNRAFMEEAEITDEDSIAAMYQAVGELPOANDTLAFLMIHL 480
 481 QRVASQPHTKMDVLANLAKVFGPTIVAAVNPDPVTMSODIKQPKVVERLLSLPLEYWS 540
 481 QRVASQPHTKMDVLANLAKVFGPTIVAAVNPDPVTMSODIKQPKVVERLLSLPLEYWS 540
 481 QRVASQPHTKMDVLANLAKVFGPTIVAAVNPDPVTMSODIKQPKVVERLLSLPLEYWS 540
 541 QPFMVQOENIDPLHVL ENSNAFSTPQTPDIKVSILGVTTPBEHQLKTPSSGSLSQVRVS 600
 541 QPFMVQOENIDPLHVL ENSNAFSTPQTPDIKVSILGVTTPBEHQLKTPSSGSLSQVRVS 600
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632
 601 TLTNTKTPRFGSKSATNLGRQGNFPAFASPMLK 632

RESULT 6

AAU69419
 ID AAU69419 standard; protein; 632 AA.

XX AAU69419;

DT 30-JAN-2002 (first entry)

XX Lung small cell carcinoma antigen #13.

XX Human: cytostatic; antitumour; lung small cell cancer antigen; tumour;

XX lung cancer.

XX Homo sapiens.

XX MO200177168-A2.

XX 18-OCT-2001.

XX 11-APR-2001; 2001WO-US011859.

XX 11-APR-2000; 2000US-0196780P.

XX 21-JUN-2000; 2000US-0213361P.

XX 01-SEP-2000; 2000US-0229763P.

XX 05-SEP-2000; 2000US-0230629P.

XX 14-SEP-2000; 2000US-0232565P.

XX 19-DEC-2000; 2000US-0257037P.

XX 08-JAN-2001; 2001US-0260796P.

XX (CORI-) CORIXA CORP.

XX Iodes MJ, Wang T, Mohamath R, Indirias CV;

XX WPI; 2002-010896/01.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

XX DR N-PSDB; AAS61859.

```
QY 121 QKSALAFNLRGQPSSSNAGNKLSTIDESGSLSDISFDPKTDSDLDWSSLVYTFKLR 180
DB 121 QKSALAFNLRGQPSSSNAGNKLSTIDESGSLSDISFDPKTDSDLDWSSLVYTFKLR 180
QY 181 EKRRETSRQFVGPPEPVKTRSIGAVDQGNESIVAKTIVVPNDGGPIEAVSTIEVP 240
DB 181 EKRRETSRQFVGPPEPVKTRSIGAVDQGNESIVAKTIVVPNDGGPIEAVSTIEVP 240
QY 241 YTRSRKRTGTLOPWNDSSTLNSROLEPRTETDSVGTPOSGNGLRHDVFSKTVIKPESC 300
DB 241 YTRSRKRTGTLOPWNDSSTLNSROLEPRTETDSVGTPOSGNGLRHDVFSKTVIKPESC 300
QY 301 VFCGRIRKFGKLSLKCRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFSQTSIP 360
DB 301 VFCGRIRKFGKLSLKCRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFSQTSIP 360
QY 361 MPTIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKYDDIHAICS 420
DB 361 MPTIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKYDDIHAICS 420
QY 421 LKDFLRNLKEPLLFRNLRAFMFAEITDEDNSIAAMYQAVGELPQANRDTLAFIMHL 480
DB 421 LKDFLRNLKEPLLFRNLRAFMFAEITDEDNSIAAMYQAVGELPQANRDTLAFIMHL 480
QY 481 QFVAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVTMSODIKRQKVERELSLPLEYWS 540
DB 481 QFVAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVTMLQDIKQPKVERELSLPLEYWS 540
QY 541 QPMWVEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLLKTSSSSLSQRVWS 600
DB 541 QPMWVEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLLKTSSSSLSQRVWS 600
QY 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
QY 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 601 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632

RESULT 7
AAU69422
ID AAU69422 standard; protein; 570 AA.
XX
AC AAU69422;
XX
DT 30-JAN-2002 (first entry)
XX
DE Lung small cell carcinoma antigen #16.
XX
KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
XX
OS Homo sapiens.
XX
PN WO200177168-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US011859.
XX
PR 11-APR-2000; 2000US-0196780P.
PR 21-JUN-2000; 2000US-0213361P.
PR 01-SEP-2000; 2000US-0229763P.
PR 05-SEP-2000; 2000US-0230629P.
PR 14-SEP-2000; 2000US-0232655P.
PR 19-DEC-2000; 2000US-0257037P.
PR 08-JAN-2001; 2001US-0260796P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Lodes MJ, Wang T, Mohamath R, Indritas CY;
XX
XX WPI; 2002-010896/01.
XX
XX N-PSDB; AAS61862.
XX
```

```
PT Lung tumor polynucleotide and polypeptides useful in therapy and
XX diagnosis of cancer especially lung cancer.
XX
PS Claim 2; Page 282-284; 295pp; English.
XX
CC The invention relates to novel isolated lung small cell cancer antigen
CC polynucleotides (I) and polypeptides (II) used in a method of detecting
CC cancer in a patient. The method is optionally performed by utilizing
CC oligonucleotides (III), where the biological sample from the patient is
CC contacted with (III), detecting the amount of polynucleotide hybridised
CC to (III) in the sample and comparing the amount of polynucleotide to a
CC predetermined cut-off value and thereby determining cancer in a patient.
CC (I), (II) or antigen-presenting cells expressing (II) is useful for
CC stimulating and/or expanding T cells specific for a tumour protein. The
CC method comprises contacting T cells with one of the components under
CC conditions to permit the stimulation and/or expansion of the cells. A
CC composition comprising (I) is useful for stimulating an immune response
CC in a patient and for inhibiting the development of a cancer especially
CC lung cancer in a patient. An isolated T cell population is useful for
CC removing tumour cells from the biological sample and for inhibiting the
CC development of cancer in a patient. AAU69407-AAU69431 represent novel
CC human lung small cell cancer antigen amino acid sequences of the
CC invention
XX
SQ Sequence 570 AA;
XX
Query Match 90.0%; Score 2919; DB 5; Length 570;
Best Local Similarity 99.8%; Pred. No. 1.2e-236;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 63 TERSALDVKLKIAHQVDEIRKQPAEADCKLERQIOLIREMLMCTSSGSIQISEBK 122
DB 1 TERSALDVKLKIAHQVDEIRKQPAEADCKLERQIOLIREMLMCTSSGSIQISEBK 60
QY 123 SALAFNLRGQPSSSNAGNKLSTIDESGSLSDISFDPKTDSDLDWSSLVYTFKLR 182
DB 61 SALAFNLRGQPSSSNAGNKLSTIDESGSLSDISFDPKTDSDLDWSSLVYTFKLR 120
QY 181 RRSRSRQFVGPPEPVKTRSIGAVDQGNESIVAKTIVVPNDGGPIEAVSTIEVP 242
DB 121 RRSRSRQFVGPPEPVKTRSIGAVDQGNESIVAKTIVVPNDGGPIEAVSTIEVP 180
QY 243 TSSRRKTGTLOPWNDSSTLNSROLEPRTETDSVGTPOSGNGLRHDVFSKTVIKPESC 302
DB 181 TSSRRKTGTLOPWNDSSTLNSROLEPRTETDSVGTPOSGNGLRHDVFSKTVIKPESC 240
QY 303 CGKRIKFGKLSLKCRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFSQTSIP 362
DB 241 CGKRIKFGKLSLKCRCRVVSHPECRCRCPICPTLIGTPVKIGEGMLADFSQTSIP 300
QY 363 PSIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKYDDIHAICS 422
DB 301 PSIVHCVNEIEQGLTETGLYRISGCDRTYKELKEFLVKTVPLISKYDDIHAICS 360
QY 423 KDFLRNLKEPLLFRNLRAFMFAEITDEDNSIAAMYQAVGELPQANRDTLAFIMHL 482
DB 361 KDFLRNLKEPLLFRNLRAFMFAEITDEDNSIAAMYQAVGELPQANRDTLAFIMHL 420
QY 483 VAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVTMSODIKRQKVERELSLPLEYWS 542
DB 421 VAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVTMLQDIKQPKVERELSLPLEYWS 480
QY 543 MWEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLLKTSSSSLSQRVSTL 602
DB 481 MWEQENIDPLHVIENSNAFSTPOTPDIKVSLGPTVTPHQLLKTSSSSLSQRVSTL 540
QY 603 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
DB 541 TLTNTPRFGSKSKSATNLGROGNFPASPMLK 570

RESULT 8
ADE60207
```

ID ADE60207 standard; protein; 628 AA.
 AC ADE60207;
 XX
 XX
 DT 29-JAN-2004 (first entry)
 DE Rat Protein AAH10715, SEQ ID NO 6113.
 XX
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SNr; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 PI
 XX Woolf C, D'ureo D, Befort K, Costigan M;
 DR WPI, 2003-268312/26.
 XX GENBANK; AAH10715.
 PT
 PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 PS Claim 1, Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNr)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPRO at
 CC ftp.wipro.int/pub/published_pct_sequences.
 XX
 SQ Sequence 628 AA;
 Query Match 84.3%; Score 2734; DB 7; Length 628;
 Best Local Similarity 84.4%; Pred. No. 5,6e-221;
 Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3;

OY 60 KAETERSALDVLLKARNQVDVEIKRQRAEADCEKLEQIQLIREMLCDTSGSIQLSE 119
 DB 61 KAETGRSALDVLLKARNQVDVEIKRQRAEACAKLEQIQLIRLILCDTSGSIQLSE 120
 OY 120 EOKSALAFINRQOPSSNAGNRLSTIDSSGILSDISFDKIDESLDMSSLVKTKLAK 179
 DB 121 EOKSALAFINRQOPSSNAGNRLSTIDSSGILSDISFDKIDESLDMSSLVKTKLAK 180
 OY 180 REKRSTSRQFVDPGPGPVKTRISGSAVDQNESIVAAITVTVVPSDGGPIEAVSTIEV 239
 DB 181 REKRSTSRQFIDGPGPVKTRISGSAVDQNESIVAAITVTVVPSDGGPIEAVSTIEV 240
 OY 240 PYWTSRRRTGTLQPNNSDSTLNSRQLEBRETEDSVGTPOQNGMRLHDFSVKTVIKPSS 299
 DB 241 PSMTSRSGKSGPLQPNNSDSTLNSRQLEBRETEDSVGTPOQNGMRLHDFSVKTVIKPSS 300
 OY 300 CVPCKRIRFGKLSLKCRDCRVVSHPECDRCPLPCIPPLTIGTIPVKIGGMLADPVSQTS 359
 DB 301 CVPCKRIRFGKLSLKCRDCRVVSHPECDRCPLPCIPPLTIGTIPVKIGGMLADPVSQTS 360
 OY 360 PMIPSTIVHCNVEIEGRGLTETGLVIRISGCDRTVELKKEFLRVKTVPLLSKVVDIHAIC 419
 DB 361 PMIPSTIVHCNVEIEGRGLTETGLVIRISGCDRTVELKKEFLRVKTVPLLSKVVDIHAIC 420
 OY 420 SLKDFLRMLKEPLTLFRLNRAFMERABITDEDSIAAMYQAVGELPQANRDTLAFMLH 479
 DB 421 SLKDFLRMLKEPLTLFRLNRAFMERABITDEDSIAAMYQAVGELPQANRDTLAFMLH 480
 OY 480 LORVASPHTKQDVANLAVFPGTTVAHAVPNDDPYTMSODIKRQPTVERLISLPLEVW 539
 DB 481 LORVASPHTKQDVANLAVFPGTTVAHAVPNDDPYTMSODIKRQPTVERLISLPLEVW 540
 OY 540 SQPMWVEQENIDPLHVIENSNAFSPQPTDIVSLGPTTPEHOLKTPSSSSLSQVR 599
 DB 541 SQPMWVEQENIDPLHVIENSNAFSPQPTDIVSLGPTTPEHOLKTPSSSSLSQVR 596
 OY 600 STLTNTTPRFGSKSKSATMIGRQNFASPMLK 632
 DB 597 N-LSKSTPRFGSKSKSATMIGRQNFASPMLK 628

RESULT 9
 AAB94223
 ID AAB94223 standard; protein; 255 AA.
 AC AAB94223;
 XX
 DT 26-JUN-2001 (first entry)
 DE Human protein sequence SEQ ID NO:14587.
 XX
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX

DR MPI; 2001-318749/34.
XX primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14587; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the combination
CC of oligonucleotide comprises at least 15 nucleotides and the combination
CC of the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 255 AA;
SQ
Query Match 36.4%; Score 1182; DB 4; Length 255;
Best Local Similarity 99.2%; Pred. No. 8.7e-91;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 397 KEKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLLFRNRAFMEEAETDDEDSIA 456
DB 20 KLFKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLLFRNRAFMEEAETDDEDSIA 79
QY 457 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKQDVANLAKVFGTTIAHVPNDPVT 516
DB 80 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKQDVANLAKVFGTTIAHVPNDPVT 139
QY 517 MSODIKROPKQKVERLLSLPLEYWSQPMWVEQENIDPLHYIENSNAFSTPQTPDIKVSILG 576
DB 140 MLODIKROPKQKVERLLSLPLEYWSQPMWVEQENIDPLHYIENSNAFSTPQTPDIKVSILG 199
QY 577 PVTTPHEQLKTPSSSSLSQVRVSTLTNTTPFGSKSKSATNLGRQGNFFASPMLK 632
DB 200 PVTTPHEQLKTPSSSSLSQVRVSTLTNTTPFGSKSKSATNLGRQGNFFASPMLK 255
RESULT 10
ID ADJ69239
ADJ69239 standard; protein; 255 AA.
AC ADJ69239;
XX 06-MAY-2004 (first entry)
XX Human heat mitochondrial protein as a therapeutic target Segid1045.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX

OS Homo sapiens.
XX
XX WO2003087768-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
XX 17-JUN-2002; 2002US-0389987P.
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
XX MPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 1045; 180pp; English.
PS This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
XX Sequence 255 AA;
SQ
Query Match 36.4%; Score 1182; DB 7; Length 255;
Best Local Similarity 99.2%; Pred. No. 8.7e-91;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 397 KEKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLLFRNRAFMEEAETDDEDSIA 456
DB 20 KLFKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLLFRNRAFMEEAETDDEDSIA 79
QY 457 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKQDVANLAKVFGTTIAHVPNDPVT 516
DB 80 AMYQAVGELPQANRDTLAFIMTHLQKVASQPTKQDVANLAKVFGTTIAHVPNDPVT 139
QY 517 MSODIKROPKQKVERLLSLPLEYWSQPMWVEQENIDPLHYIENSNAFSTPQTPDIKVSILG 576
DB 140 MLODIKROPKQKVERLLSLPLEYWSQPMWVEQENIDPLHYIENSNAFSTPQTPDIKVSILG 199
QY 577 PVTTPHEQLKTPSSSSLSQVRVSTLTNTTPFGSKSKSATNLGRQGNFFASPMLK 632
DB 200 PVTTPHEQLKTPSSSSLSQVRVSTLTNTTPFGSKSKSATNLGRQGNFFASPMLK 255
RESULT 11
AAU32069
ID AAU32069 standard; protein; 256 AA.
XX AAU32069;
AC
XX 18-DEC-2001 (first entry)
DT

XX DE Novel human secreted protein #2560.
 XX XX
 XX Human: vaccination; gene therapy; nutritional supplement;
 XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX OS Homo sapiens.
 XX MO200179449-A2.
 XX PD 25-OCT-2001.
 XX PF 16-APR-2001; 2001WO-US008656.
 XX PR 18-APR-2000; 2000US-00552929.
 XX PR 26-JUN-2001; 2001US-00770160.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX PI WPI; 2001-611725/70.
 XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 XX PT vaccination, testing and therapy.
 XX PS Claim 20; Page 551; 765pp; English.
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU2510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 XX SQ Sequence 256 AA;
 Query Match 30.0%; Score 971.5; DB 4; Length 256;
 Best Local Similarity 84.0%; Pred. No. 4.9e-73;
 Matches 205; Conservative 3; Mismatches 27; Indels 9; Gaps 4;
 QY QTSMPISIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLRVKTVPLLSKYDDIH 416
 DB 1 QTSMPISIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLRVKTVPLLSKYDDIH 60
 QY 417 AITSLIKDPLRNKEPPLTLRLNRAFEAAETDEDSNIAAMYQAVGELFOANRDTLAF 476
 DB 61 AITSLIKDPLRNKEPPLTLRLNRAFEAAETDEDSNIAAMYQAVGELFOANRDTLAF 120
 QY 477 MHLQVVAOSPHTKMDVANLAKVGPITYAHAVPNPDVPMQDIR-OPKVERLLSLP 535
 DB 121 MHLQVVAOSPHTKMDVANLAKVGPITYAHAVPNPDVPMQDIR-OPKVERLLSLP 180
 QY 536 L-EYMSQFMWVEOE--NIDPLHVIENSNAFTPTGPDIKV---SLAGPVTTPHEQLK 587
 DB 181 LMEYMFESFMDGEGGTFPLPLVINSNMFSTPQPDICAVPGGGLCHFTAGAEAIQK 240
 QY 588 TPSS 591
 DB 241 GPPS 244

RESULT 12
 ABB68056
 ID ABB68056 standard; protein; 625 AA.
 XX AC ABB68056;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 30960.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN MO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX PI WPI; 2001-656860/75.
 XX DR N-PSDB; ABL12159.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
 XX PT interactions.
 XX PS Disclosure; SEQ ID NO 30960; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 XX capable of detecting 1000 or more genes from Drosophila. The invention is
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
 XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 XX ABB72072). The sequence data for this patent did not form part of the
 XX printed specification, but was obtained in electronic format directly
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 625 AA;
 Query Match 26.6%; Score 864; DB 4; Length 625;
 Best Local Similarity 35.1%; Pred. No. 2.4e-63;
 Matches 228; Conservative 110; Mismatches 225; Indels 86; Gaps 21;
 QY 4 MMLNVANLFEQIVRVEITSEGN-EVQFIQLKDPEDPKKQQRTHDELQKXDLMKAE 62
 DB 1 MALISALASFDLRLRCMQVLTIDGTPPEEFRLFLMEQHEKCAGYAAETARLONELDKSL 60
 QY 63 TERSALDVLKILKARNQVDEIRKQPAEADCEKLEIOLIREMLMCDTSGISLSEBK 122
 DB 61 TKMGDEGLFLPHARRIDIEIKARQAEHERAMESKINAAVADLHNEH---LNNEFR 116
 QY 123 SALAFINRQOPSS---NA--GNKRLSTIBESGSLIDISFDKT-DSLDMDSLVKT 174
 DB 117 DKLAFLHT-LPSRRKRSINAAVREDKSYGDINSTGSLISLDSITISEDDFLD-----VRT 170
 QY 175 FLKKREKRKRSRQGV-----DGPGRPVKTR--SIGSAVD----- 209
 DB 171 SK-SMREHRPSLPKQIPEVGKRSRLSTGLNGSNSGTPPTTGKSRSSVGIGVEQHTVD 229
 QY 210 --QGNESIVAKTTVTPNDG-GPIEAVSTIETVTPYTRSRRTGTLQPNMSDSTLNSROL 266

XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
DR MPI; 2001-639362/73.
XX N-PSDB; AAS74417.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 40589; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for creating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 665 AA;
SQ
Query Match 19.1%; Score 618; DB 4; Length 665;
Best Local Similarity 46.9%; Pred. No. 1.4e-42;
Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;
QY 255 WNSDSTLNSRQLEPRRTSDSVGTPOSGMRLHDPVSKTVIRPESCVPCKRIKFGKLSL 314
DB 369 WIKD--LNVRPRTIKTLENTLGNITDIDGMG-KDFMSKT--PKMATKTKDKMDLIOL 422
QY 315 KCRDCRVSHPECRDRCPLPCITPLIGTPVKIG-----EGMLADPVSQTSMPISIVNH 368
DB 423 KSFRC-----TAKETTRVNRQPTWEKIFATYSSD-----KGLISR 459
QY 369 CNEIEIQ-----RGLTETGLY-----RISGCDR--TVKELNEK-FLRV 403
DB 460 IYVELKQIYKKKTNNPIKKWTNMDNRHFSKEDIYAAKKHKKSSSLPAIREMDIKTMYR 519
QY 404 KTVVPL-----SKYDDIHAISGLKDFLNLKEPLTLRLNRAFMEEAITDEDN 453
DB 520 HLTPVIAIIRKSGNNSKYDDIHAISGLKDFLNLKEPLTLRLNRAFMEEAITDEDN 579
QY 454 STAAWQAVGELQOANRDTLAFIMHLORYAOSPHRTKMDVANKVFGPTIVAAVNPDP 513
DB 580 SISAMQAVGELQOANRDTLVFLMIHLORYAOSPYTRKMNVAALVFGSTIVAAVNPDE 639
QY 514 PVTMSQDIKQPKRVVERLSLPLEYW 539
DB 640 PVTMLQDIKQPKRVVERLSLPLEYW 665
RESULT 15
ABG19904

ID ABG19904 standard; protein, 1086 AA.
XX
XX AC ABG19904;
XX
XX 18-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #19895.
XX
XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
DR MPI; 2001-639362/73.
XX N-PSDB; AAS84091.
XX
DR New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX PS Claim 20; SEQ ID NO 50263; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for creating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1086 AA;
SQ
Query Match 19.1%; Score 618; DB 4; Length 1086;
Best Local Similarity 46.9%; Pred. No. 3.2e-42;
Matches 153; Conservative 35; Mismatches 68; Indels 70; Gaps 11;
QY 255 WNSDSTLNSRQLEPRRTSDSVGTPOSGMRLHDPVSKTVIRPESCVPCKRIKFGKLSL 314
DB 790 WIKD--LNVRPRTIKTLENTLGNITDIDGMG-KDFMSKT--PKMATKTKDKMDLIOL 843
QY 315 KCRDCRVSHPECRDRCPLPCITPLIGTPVKIG-----EGMLADPVSQTSMPISIVNH 368
DB 844 KSFRC-----TAKETTRVNRQPTWEKIFATYSSD-----KGLISR 880
QY 369 CNEIEIQ-----RGLTETGLY-----RISGCDR--TVKELNEK-FLRV 403

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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:08:37 ; Search time 43 Seconds
(without alignments)
1414.163 Million cell updates/sec

Title: US-09-881-736a-2

Perfect score: 3243
Sequence: 1 MDTMMLNVNLFPEQLVRRVE.....SKSATNLGRQGNFASPMUK 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: pirl:.*
2: pirl2:.*
3: pirl3:.*
4: pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	2 D59430	Rac GTPase activat
2	547.5	16.9	681	2 T23454	hypothetical prote
3	477	14.7	383	2 B48122	GTPase-activating
4	477	14.7	384	2 A48122	GTPase-activating
5	348	10.7	1980	2 S54307	myosin heavy chain
6	334	10.3	2022	2 A59256	myosin-Ixb [simila
7	329	10.1	334	2 S29128	N-chimerin - rat
8	322	9.9	289	2 S08242	N-chimerin - human
9	320	9.9	239	2 A43953	N-chimerin - commo
10	308	9.5	695	2 T39954	probable gtpase ac
11	301	9.3	1261	2 E59430	PTPL1-associated R
12	294	9.1	295	2 S29956	beta-chimerin - ra
13	294	9.1	443	2 B53764	beta2-chimerin, ce
14	293.5	9.1	466	2 A53764	beta2-chimerin, ce
15	291	9.0	970	2 D59435	Gem-interacting pr
16	290.5	9.0	814	2 F59430	GTPase regulator a
17	286.5	8.8	1944	2 A59438	KIAA1424 protein l
18	285.5	8.8	1165	2 D59433	C. elegans protein
19	282	8.7	859	2 A49307	98K GTPase-activat
20	281	8.7	813	2 B47485	ABR protein 2 - hu
21	280	8.7	822	2 A47485	ABR protein 1 - hu
22	280.5	8.6	733	2 S44876	CC21.4 protein - C
23	275.5	8.5	1271	1 TVHUBR	bcr (breakpoint c)
24	270.5	8.3	1397	1 T46354	hypothetical prote
25	270.5	8.3	2548	2 E59435	myosin IXA limort
26	269.5	8.3	735	2 A59434	KIAA1501 protein l
27	267.5	8.2	2626	2 T31099	myosin-RhoGAP proc
28	260.5	8.0	802	2 H59434	oligophrenin 1, Rh
29	258	8.0	903	2 T00705	N-chimerin homolog

30	253.5	7.8	1846	2 T33079	hypothetical prote
31	247.5	7.6	655	2 A59430	hypothetical prote
32	247	7.6	863	2 T27958	hypothetical prote
33	245	7.6	1445	2 A59437	KIAA1204 protein l
34	240	7.4	969	2 T36478	RhoGAP/LIM domain
35	238	7.3	974	2 E59434	Rho GTPase activat
36	232	7.2	666	2 S29349	hypothetical prote
37	231.5	7.1	647	2 A57467	RalBP1 - rat
38	231	7.1	818	2 A59433	KIAA0672 protein l
39	229.5	7.1	574	2 T29005	hypothetical prote
40	229.5	7.1	655	2 F59435	rala-binding prote
41	229	7.1	634	2 T27959	hypothetical prote
42	228.5	7.0	837	2 T19825	hypothetical prote
43	222.5	6.9	892	2 T40040	GTPase-activator p
44	221.5	6.8	316	2 T46471	hypothetical prote
45	217	6.7	512	2 E59437	F02569_2 protein l

ALIGNMENTS

RESULT 1

D59430
Rac GTPase activating protein 1 [imported] - human
C/Species: Homo sapiens (man)
C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #ext_change 09-Jul-2004
C/Accession: D59430
R:Kawashima, T.; Kitamura, T.; Nosaka, T.; Hirose, K.
submitted to GenBank, December 1999
A/Description: Homo sapiens Rac GTPase activating protein 1 (RACGAP1), mRNA.
A/Reference number: D59430
A/Accession: D59430
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-632 <KAM>
A/Cross-references: UNIPROT:Q9P2W2; GB:NP_037409; PIR:g7019433; PIR:NP_037409.1

Query Match 100.0%; Score 3243; DB 2; Length 632;

Best Local Similarity 100.0%; Pred. No. 1.9e-197;

Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDTMMLNVNLFPEQLVRRVEILSEGNVQFIQAKDFEDPRKKWQRTDHELKYYKDLMMK 60
DB	1	MDTMMLNVNLFPEQLVRRVEILSEGNVQFIQAKDFEDPRKKWQRTDHELKYYKDLMMK 60
QY	61	AETERSALDVKUKHAANOVDVEIKRQRAADCEKLERQIQILREMLMCDTSGSIQLSSE 120
DB	61	AETERSALDVKUKHAANOVDVEIKRQRAADCEKLERQIQILREMLMCDTSGSIQLSSE 120
QY	121	QKSALAFNLRGQPSNNAGNKRSLTIDSGSILSDISPKTDBSLDMSLIVTFKLR 180
DB	121	QKSALAFNLRGQPSNNAGNKRSLTIDSGSILSDISPKTDBSLDMSLIVTFKLR 180
QY	181	EKRRTSRQFVDPGPGPVKKTRSIGAVDQNESIVAKTTVVVNDGPIEAVSTIEYVP 240
DB	181	EKRRTSRQFVDPGPGPVKKTRSIGAVDQNESIVAKTTVVVNDGPIEAVSTIEYVP 240
QY	241	YWTRSRRTKGTLOPMNSDSTLNSROLEPRTEDSVCTPOSGNGMRLLHDPFSKVIKPESC 300
DB	241	YWTRSRRTKGTLOPMNSDSTLNSROLEPRTEDSVCTPOSGNGMRLLHDPFSKVIKPESC 300
QY	301	VPCGRKIKFGKSLKCRDRCVVSHPCECRDRCPLPCLITLIGTPVKIGEGMLADFVQSTSP 360
DB	301	VPCGRKIKFGKSLKCRDRCVVSHPCECRDRCPLPCLITLIGTPVKIGEGMLADFVQSTSP 360
QY	361	MPSIVVHCNVEIEQGLTETGLYRISGCDRTYKELKEKFLRVKTVPLLSKVDVIAICS 420
DB	361	MPSIVVHCNVEIEQGLTETGLYRISGCDRTYKELKEKFLRVKTVPLLSKVDVIAICS 420
QY	421	LKQDFLRNKEPLTFLRLRAFMFAEITDSDNSIAAMYQAVGELPOANRDTLAFIMIH 480
DB	421	LKQDFLRNKEPLTFLRLRAFMFAEITDSDNSIAAMYQAVGELPOANRDTLAFIMIH 480

Qy	481	QRAVASPHTMDVANAIAKAFEGPTIAVAHVPNDPVTMSQDIKROPKVERRLSLPLEYMS	540
Qy	481	QRAVASPHTMDVANAIAKAFEGPTIAVAHVPNDPVTMSQDIKROPKVERRLSLPLEYMS	540
Db	481	QRAVASPHTMDVANAIAKAFEGPTIAVAHVPNDPVTMSQDIKROPKVERRLSLPLEYMS	540
Qy	541	QEFMVVROENIDPLAHTIENNSASTPOTPIKXSLGLPVTTEHOLKTPSSSLSCBVR	600
Qy	541	QEFMVVROENIDPLAHTIENNSASTPOTPIKXSLGLPVTTEHOLKTPSSSLSCBVR	600
Db	541	QEFMVVROENIDPLAHTIENNSASTPOTPIKXSLGLPVTTEHOLKTPSSSLSCBVR	600
Qy	601	TLTIKATPFGSKSKSATNLGROGNFPASPMK	632
Qy	601	TLTIKATPFGSKSKSATNLGROGNFPASPMK	632
Db	601	TLTIKATPFGSKSKSATNLGROGNFPASPMK	632

RESULT 2
T23454

hypothetical protein K08E3.6 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23454
R/McMurray, A.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19743
A/Accession: T23454
A/Status: preliminary; translated from GE/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-681 <WLL>
A/Cross-references: UNIPROT:Q9XUS9, EMBL:Z81568, PIDN:CAB04593.1, GSPDB:GN00021, CESP:K08E3
A/Experimental source: clone K08E3
C/Genetics:
A/Gene: CESP:K08E3.6
A/Map position: 3
;Introns: 36/1/, 73/2/, 237/3/, 361/3/, 612/3

[illegible][illegible]

RESULT 3
PAGE 111

C:Species: Drosophila melanogaster
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997
 C:Accession: B48122
 R:Agnew, M.; Roder, L.; Voja, C.; Griffin-Shea, R.
 M.Ol. Cell. Biol. 12, 5111-5122, 1992.
 A:Title: A Drosophila rotund transcript expressed during spermatogenesis and imaginal di
 A:Reference number: A48122; MID:93024458; PMID:1406685
 A:Accession: B48122
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-383 <GN>
 A:Note: sequence extracted from NCBI backbone (NCBIN:115662, NCBI:P.115663)
 C:Genetics:
 A:Gene: FlyBase:rn
 A:Cross-References: FlyBase:Fgmn0003263

	Query Match	14.7%;	Score 477;	DB 2;	Length 383;
	Best Local Similarity	40.7%;	Pred. No. 8.9e-23;		
	Matches 110;	Conservative 44;	Mismatches 102;	Indels 14;	Gaps 6;
QY	279	QSNKG-MRLHDFVSKT-VIKPESCVPGCKRIKFGKSLKRCDRRVVSHPECRPCLPCT	336		
Db	78	QSHSGGLREINFIKSYNYVNGCVHCRKRIKIPAMASLRCRAOPLRHIGCCQRLTVNCI	137		
QY	337	P-FLIGTPVXIGEGMLADFVSQSPMIPSIVHVCVEIEORGLTETGLYRISGCDRTVKE	395		
Db	138	PQPIQIGTK---RGCLSDVAPRVAPWVPLIVHCVTEIEARGLQDSGLYRVSSSTREKCKR	193		
QY	396	LKEKFLRVKTVPLISKYDDIHAI CSLKDPFLRNLKPELTLFLRRAFMEEAAETDEBNST	455		
Db	194	LRRKLLRGKSTPHLGN-KDTHLLCCCVKDFQLVHPLPIYHRRPFEEATRHEDRLAVE	252		
QY	456	AAAYQAVGELPQANRDPTLAFLMHLQRFVQAQSPETKMDVANLAKVFGTIIYAHAHVPNEDPV	515		
Db	253	MAVYLAFLBELHQHARDPTIAYLMHMQKIAESPAVRMTVNNLAVIAPATLFG-----DL	306		
QY	516	TMSODIKRQPKYVERLLSLPLEYWSQPMY	545		
Db	307	LTLLENVTVQRVLKVLKLLMPAGFWSQPLEY	336		

RESULT 4

Grape-seed-activating protein Rac homolog, splice form pcl.7 - fruit fly (*Drosophila melanogaster*)
 C/Species: *Drosophila melanogaster*
 C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A48122
 R/Agmel, M., Roder, L., Voja, C., Griffin-Shea, R.
 Mol. Cell. Biol. 12, 5111-5122, 1992
 A/Title: A *Drosophila* retund transcript expressed during spermatogenesis and imaginal disc development
 A/Reference number: A48122; MUID:33024458; PMID:140665
 A/Accession: A48122
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-384 <AGN>
 A/Cross-references: UNIPROT:P40809
 A/Note: sequence extracted from NCBI backbone (NCBI:115660, NCBI:115661)


```

Qy 71 ----KTKARNVDVEIKRQRAEADCEKLEROIQIIREMLMCDISGSIQISEEQKSALA 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1459 PEGOOHRHAAAGE-----KRTKEPGGKGKKNNRVKI-----GKITVEKMESEVF 1502
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 127 FLNRQPPSSNNGKRLSTIDE-SGSIISDISFDKDESLDWDSSLVKTFKLKKQEKRS 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1503 ----ROITAN-----ELKYLDEPLKINDLSQKTP-----TESLFIENAEKERS 1545
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 186 TSROFDPGPPGVKTRISGSAVDQGNESIVAKTIVTVNPDGPPEAVSTIET-VPYMT 244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1546 NIKMYVSVPNGKI-----HVGVDLMENYQIVVSNLATERGQDQTNVLMFQSLDEFIR 1601
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 245 SRKKTGTLQPNWSDSTLNSRQLEPRTETDSVGTPOSGMRLHDPVSKTVIKPESCVPG 304
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1602 GYTK-----NDPEFVKOSKQKKRKOERAVOEHNQ-----HVFASYQVSIPOSCQCL 1650
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 305 KRIKKGKLSIKGRDCRVSHPECRDRCPICPTL--IGTP--VKIGE--GMLDPFVQSPT 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1651 SYIMLMDKRLDSCVCKMTCHKCKVHKIQSHCSYTGKCKEPPGAPGPHFQVCDSTSDKA 1710
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 361 MIPSIYVHCNEIEQRLETETGLYRISGCDRTVKELEKELFNVKTVPLLSKYDD--IHAI 418
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1711 SVPIVLEKLEHVENHGLTTEGLYRKSGANTRRELQ---ALQTDPAVKKLENFPIHAI 1767
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 419 GLLLDLFLNLKEPLITFPLNRAFMFAEITBEDNSIAAMYQAVGELPQANDTIAFLMI 478
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1768 TGVLKQMLEPEPLMTFAQYGFLEAVELPEKQEOIAIVAVLEHLEPANNHSLERLIF 1827
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 479 HIGQVA-QSPHTKMDVANKVFGPPIVAHAVNPDPVMSODIKQKQPVVERLLSLPE 537
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1828 HLYKVALLEDVNRMSGALAIIFAPCLL-RCPDNSDPLTSMKDVLEKITTEVEMLLEQKR 1886
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 538 YVSQFMVVEQENIDPLHVEN-----SNAFSTPQTPD-----IKVSLGPLYT 579
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1887 KKK---VMEERISQLEABESIAFRRLSLRQNNANSPRTREBAGAGRLITTSRVP-- 1940
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 580 TPEHOLLKTPSSSSLSQVRST-----LTKNTER 608
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1941 SPSTRMLALGSWRSAALRTRGTRPARPGARALRRPR 1980
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
S29128
N:Chimerin - rat
N:Alternate names: GTPase-activating protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S29128; S25152
R:Lim, H.H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.
Biochem. J. 287, 415-422, 1992
A:Title: Developmental regulation and neuronal expression of the mRNA of rat n-chimerin
A:Reference number: S29128; PMID:93074974; PMID:1445199
A:Accession: S29128
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-334 <Lim>
A:Cross-references: EMBL:P30337; EMBL:X67250; NID:G55939; PID:G55940
R:Lim, H.; Michael, G.J.; Smith, P.; Lim, L.; Hall, C.
submitted to the EMBL Data Library, July 1992
A:Description: Rat n-chimerin a p21rac GAP:cDNA sequence developmental regulation and n
A:Reference number: S25152
A:Accession: S25152
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-334 <Lim>
A:Cross-references: EMBL:X67250; NID:G55939; PID:CAA47672.1; PID:G55940
F:81-130/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match 10.1%; Score 329; DB 2; Length 334;
Best Local Similarity 32.4%; Pred. No. 1, 7e-13;
Matches 91; Conservative 46; Mismatches 118; Indels 26; Gaps 8;

```

```

Qy 259 STLNSRQLEPRTETDSVGTPOSGMRLHDPVSKTVIKPESCVPGKRIKRGKLS--LKC 316
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 ATLKENEOIPKYE-----KVHNEFVHTFRGPHWCEYA-NFMGLIAGVVC 111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 317 RDCRVVSHPECRDRCPICPTLIGTPVKIGEMLADFVSQSPMIPSIYVHCNEIEQR 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 ADCGLNVHKQCSKMPNDCKPDLKHVK-KVYSCDLITLVKAITRPMVYDMCIREISER 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 377 GLTETGLYRISGCDRTVKELEKELR--VKTVPLLSKYDDIHAIQSLKDFLRNKEPLL 434
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 GLNSGLYRVSGFSDLIEDVKMAFDRDEKADISVMYEDINIIGALCLYFRDPIPLI 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 435 TFLNRAPFMEAEITDEDNSIAAMYQAVGELPQANDTIAFLMIHLQRYAOSPHRK---M 491
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 TYDAVPKPLESAKIDPDEQLETLHEALRSLPPACETLRIMAHLEKRV--TLHEKENIM 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 492 DVANLAKVGPPIVAHAVNPDPVMSODIKQKQPVVERLL 532
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 SAEINIGIVGPILMS--PELDPMALNDIRQRLVVELLI 327
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
S08242
N:Chimerin - human
N:Alternate names: GTPase-activating protein
C:Species: Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Mar-2004
C:Accession: S08242
R:Hall, C.; Montfries, C.; Smith, P.; Lim, H.H.; Kozma, R.; Ahmed, S.; Vanniasingham, V.;
J. Mol. Biol. 211, 11-16, 1990
A:Title: Novel human brain cDNA encoding a 34,000 Mr protein n-chimerin, related to b
A:Reference number: S08242; PMID:90133942; PMID:2299665
A:Accession: S08242
A:Molecule type: mRNA
A:Residues: 1-299 <Hall>
A:Cross-references: EMBL:X51408; NID:G35012; PID:CAA35769.1; PID:G35013
F:46-95/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match 9.9%; Score 322; DB 2; Length 299;
Best Local Similarity 32.0%; Pred. No. 4e-13;
Matches 90; Conservative 48; Mismatches 117; Indels 26; Gaps 8;

Qy 259 STLNSRQLEPRTETDSVGTPOSGMRLHDPVSKTVIKPESCVPGKRIKFKLS--LKC 316
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 ATLKENEOIPKYE-----KIHNFVHTFRGPHWCEYA-NFMGLIAGVVC 76
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 317 RDCRVVSHPECRDRCPICPTLIGTPVKIGEMLADFVSQSPMIPSIYVHCNEIEQR 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 ADCGLNVHKQCSKMPNDCKPDLKHVK-KVYSCDLITLVKAITRPMVYDMCIREISER 135
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 377 GLTETGLYRISGCDRTVKELEKELR--VKTVPLLSKYDDIHAIQSLKDFLRNKEPLL 434
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 GLNSGLYRVSGFSDLIEDVKMAFDRDEKADISVMYEDINIIGALCLYFRDPIPLI 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 435 TFLNRAPFMEAEITDEDNSIAAMYQAVGELPQANDTIAFLMIHLQRYAOSPHRK---M 491
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 196 TYDAVPKPLESAKIDPDEQLETLHEALRSLPPACETLRIMAHLEKRV--TLHEKENIM 253
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 492 DVANLAKVGPPIVAHAVNPDPVMSODIKQKQPVVERLL 532
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 NAEINIGIVGPILMS--PELDPMALNDIRQRLVVELLI 292
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
A43953
N:Chimerin - common canary
N:Alternate names: protein kinase C homolog [misidentification]; song control circuit pr
C:Species: Serinus canaria (common canary)
C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 15-Mar-2004
C:Accession: A43953
R:George, J.M.; Clayton, D.F.
Brain Res. Mol. Brain Res. 12, 323-329, 1992
A:Title: Differential regulation in the avian song control circuit of an mRNA predicting

```



```

OY 407 PLKSKVD-----DI-----HAICSLKDFRLNKEPFLRLNRAFMPEAAE-----TTDE 451
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 717 KLCALALENGMLVADISERSHDICDVLKLYLRQLPEPPIFLRKYKEFDIAKEIQHYNEE 776
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 452 DNS-----IAAMYQAVGELLPOANDRTLAFIMLTHLORVA-QSPEHTK 490
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 777 QETKKNLSIEDKKEMPMCEINRIILKSKDILROLPASNPNSLHFLIYHLKRVADHAENK 836
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 491 MDVANIIAKVEGPTIYAHAVNPD--PYTMSQ--DIKQPKVEELLISPLEYWSQFM--- 543
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 837 MNSKNLGYTFEPPSLIR---PRPQTAFITISLAAYSNQARVEFLIT-----YSQKFDG 888
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 544 -MVEQENIDPLHYIENS---NAFSTPQTDFDIKAVLGGVYTPPEHOLKTPBSSSLISQORV 599
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 889 SLOPQDVWCSIGVUDQCGFPKPLLSPEERDIERSMKSLFFSKEDIDHTSESESKIFERAT 948
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 600 STLTKNTPRFGSKSKSATNLGR 621
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 949 S-----FEESERKQNALGK 962
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 12
S29956
beta-chimerin - rat
N/Alternate names: GTPase-activating protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: A45485, S31398, S29956
R/Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 268, 3813-3816, 1993
A/Title: Germ cell beta-chimerin, a new GTPase-activating protein for p21rac, is specific
A/Reference number: A45485; MUID:93179371; PMID:8440677
A/Accession: A45485
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-295 <LEU>
A/Cross-references: UNIPROT:003070; EMBL:X69489; NID:957526; PIDN:CAA9244.1; PID:957527
A/Experimental source: testis
A/Note: sequence extracted from NCBI backbone (NCBI:P12571)
R/Leung, T.; How, B.E.; Manser, E.; Lim, L.
submitted to the EMBL Data Library, November 1992
A/Description: Germ cell beta-chimerin, a new GTPase-activating protein for p21rac, is
A/Reference number: S31398
A/Accession: S31398
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-295 <LEU>
A/Cross-references: EMBL:X69462; NID:955816; PID:955817
F/42-91/Domain: protein kinase C zinc-binding repeat homology <X2>

	Query Match	9.1%; Score 294; DB 2;	Length 295;
	Blast Local Similarity	29.3%; Pred. No. 2.3e-11;	
	Matches	81; Conservative	52; Mismatches 111; Indels 32; Gaps 8;
Qy	285 RLHDFVSKTVIKPSCVPCGGRIRKFGKLS--LKCRDRVVSHPECRDRCPLCIPTLIGT	342	
Dd	40 KTHNFKVHTFPGPHMCEYCA-NFMWGIIAQVRSDGLGNHNKCCHVPNDQPDLRKI	98	
Qy	343 PVKLGEGMLADPFVSOTSPMIPSIYVHCYNELFQGSLTETGLYRISGCDRYVKELKEKFLR	402	
Dd	99 K-KAYCCDLTLIVKAHNTQRPMVVDICIRELEAGLSEGGIYRVSGTEHIEDTKAFDR	157	
Qy	403 VKTVPLLSKVD-----DIHAICSLKDPIRLNKLPFLTRLMRAEMEAARITDEENSI	455	
Dd	158 DG-----EKADISANIYPDINITTGALKLYPRDIPILITYDYTKTEIAAKISNAERL	212	
Qy	456 AAMYGAVGELEPOANRDTLAPLMHLORVAOSPHRK-MDVANLAKVFPTLVAAHVNPDP	514	
Dd	213 EAVHEVLMLTPRAYETRLRYMIHLKKVTVMNEKNONMAEELGVFPETLM--RRPEDST	270	
Qy	515 VTMSSODIKQPKVVERLLSLPLEYWSQPMVEQENI	550	

```

DB          271 LTTLHDMRYOKLIWO-----ILLIENEDV 293

RESULT 13
B53764      beta2-chimerin, cerebellar - rat (fragment)
N.Alternate names: GTPase-activating protein
C.Species: Rattus norvegicus (Norway rat)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 04-Apr-2004
C.Accession: B53764
R.Leung, T.; How, B.E.; Manser, E.; Lim, L.
J. Biol. Chem. 269, 12888-12892, 1994
A.Title: Cerebellar beta2-chimerin, a GTPase-activating protein for p21 Ras-related Rac
A.Reference number: A53764; MUID:94230370; PMID:815705
A.Accession: B53764
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-443 <LEU>
F.i34-114/Domain: SH2 homology <SH2>
F.i190-239/Domain: protein kinase C zinc-binding repeat homology <K2>

```

Query Match	9.1%;	Score 294;	DB 2;	length 443;
Best Local Similarity	29.3%;	Pred. No. 4.1e-11;		
Matches	81;	Conservative	52;	Mismatches 111; Indels 32; Gaps 8;
QY	285	RLLDFVSKYIVKESCYPCGGRKIKFGKLS--LKCRDRCVVSHEPCDRCLPCLPIPLTIGT	342	
Db	188	KTNHFKVHTFRGPRWCYCQA-NFMWGLIAGVRCSCGLVNHQCSHWPNDDQPLDKRI	246	
QY	343	PKVIGEGMLDFVQSQTSPMIPSIIVHCVNEIEORGLETETLYRISGCDRTVKEJKEKFLR	402	
Db	247	K-KYCCGLDTLVKANHQTGRPMVVDICIRIEIENRGLKSESLYVSGFTEHIEDVKNAPDR	305	
QY	403	VKTYVPLLSKYD-----DIIHALCSLLKDXLRLNKEPBLTFLRNAPMEAAETTDENSI	455	
Db	306	DG-----EKADISANIYPIDNIITTGALKLYFRDLPPIITLYDYRSKFEAKISNADERL	360	
QY	456	AAMYQAVGELPQANRDITLAFMLTHLQRFVQSPHPTK--MDVANLAKVNGPITIIVAAHVNPDP	514	
Db	361	EAVHEVLMLLPRAHYETLRYLTMHLKKVTINERKDNIMANENLIGVQPTLM--RPEDST	418	
QY	515	VYMSQDILKQPKVYVERLSLPLEYWSQPMVVEQENI	550	
Db	419	LTLIHDNRKYQLIVQ-----LIIENEDV	441	

```

RESULT 14
A:53764
beta2-chimerin, cerebellar - human
N:Alternate names: GTPase-activating protein
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A53764
R:Leung, T.; How, B.B.; Manser, E.; Lim, L.
J. Biol. Chem. 269, 12888-12892, 1994
A>Title: Cerebellar beta2-chimerin, a GTPase-activating protein for p21 Ras-related Rac
A:Reference number: A53764; MUID:94230370; PMID:8175705
A:Accession: A53764
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-466 <LEU>
A:CROSS-references: UNIPROT:P52757; GB:L29126; NID:g457229; PIDN:AAA191.1; PID:g457230
F:157-137//Domain: SH2 homology <SH2>
F:213-262//Domain: protein kinase C zinc-binding repeat homology <K2>

Query Match          9 1%: Score 293.5; DB 2; Length 466;
Best Local Similarity 25.7%: Pred. No. 4.7e-11;
Matches 98; Conservative 66; Mismatches 155; Indels 63; Gaps 12;

Oy 199 KKTSSISAADQGNESIVAKTTVTVPNDGGPIAVSTIEVP-----YWTSRRRKTGTL 252
Db 116 KRFSIHDLVTGILTYIETKAA-----EYISKMTNPIYHIGYATLLREKV--- 164

```


QY 253 QPNSSTLNSRLQLEP-----TETDSVGTPOSNGM-----RLHDPVSKT 293
 DB 165 -----SRRLSRSGNREPKTNVTHEHTAVKISSLYRRALITNDNHNFKYKTHKVT 219
 QY 294 VIKESCVPCGKRIKKGKLS--LKCRDVRVSHPECDRCPLPCIPTLITPVKIGGML 351
 DB 220 FRGPHHCEYCA-NFMWGLAQGVRCSDCGLNHKKQSKHVPNDQCPDLKRIK-KVYCCDL 277
 QY 352 ADFVSQTSPIPSIVHCVNIEIQRGLTETGLYRISGCDRTVKELEKFLR--VKTVPFL 409
 DB 278 TTLVKAHNQRPVNVVICIREIARGKSGLYRVSGFTIHIEDVYMAFRDDEKADISA 337
 QY 410 SKYDDIHAICSLIKDPLRNKEPULTFRLNRAFMEEAETDEDNLSAAMTQAVGELPQAN 469
 DB 338 NVYPDINIITGALKLYFRDLPPIVITYDYTSKEFIDAKISNADERLEAVEHVLMLPPAH 397
 QY 470 RDTLALMTLHLOVAVASPHTK-MDVANLAKVPGPTVAHAVPNPDVPTMSQDIKROPKY 528
 DB 398 YETLRKLTMLHKKVTNMEKDNFMNAENLGIVFGPTLM--RPPEDSTLTTLHDMRYOKLIV 455
 QY 529 ERLLSLPLEYWSQPMWVEQENI 550
 DB 456 Q-----ILINEDV 464

RESULT 15
 D59435
 Gem-interacting protein (imported) - human
 C.Species: Homo sapiens (man)
 C.Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
 C.Accession: D59435
 R.Arresta, S.; Beranger, F.; Berger, R.; de Gunzburg, J.
 submitted to Genbank, November 2000
 A.Description: GMIP, a Gem interacting protein.
 A.Reference number: D59435
 A.Accession: D59435
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-970 <ARB>
 A.Cross-references: UNIPROT:Q9P107; GB:NP_057657; PID:g7706107; PIDN:NP_057657.1

Query Match 9.0%; Score 291, DB 2; Length 970;
 Best Local Similarity 22.6%; Pred. No. 1,9e-10;
 Matches 188; Conservative 112; Mismatches 273; Indels 260; Gaps 40;

QY 13 EOLVRVBILSEGENVQFIQAKDFEDERK--W--QRDHELQKYLKDLMAKETERSA 67
 DB 81 EELDLRL-IRTKGVDAALRYAKTWSRYAKELLAMTEKRASYELEPAKSTMTKTAENGVK 139
 QY 68 LDYK-----LKH-----ARQVDVE-----82
 DB 140 IQQSHMPLQIYITLFLHDLISLGLAMETVAQOKDYQPLAKRTIEIKMKRKEPKQW 199
 QY 83 IKRQRAEDCEKLER-QIQLIR--EMLKDTSGSIQISEOKSALAFLNRGQPSNNAG 139
 DB 200 MKEOKMNEAVQALRRARQLQYVORSIEDLRARSOGSPEDSAPQAS-----FGPSKQ 250
 QY 140 NKRSLTIDSGSLDISIPKTDSESLDMSLVKTFLLKRE---KRRST--RQFV-D 192
 DB 251 ERRRRSRREBQA-----KAQEAELVQACVREANARQODLEIAKQRTVSHVRKLVQ 302
 QY 193 GPPGPKVTKRSI-----GSAVDQGNESIVAKTIVTPVNDG-----PIE 231
 DB 303 GDEVLARVLTSLFLGLGAQAGRPRAFAALAECCAPPEPQRYQGFVRLARPEAPPPPP 362
 QY 232 AVSTITVYWTNS-----RKKTGTLQ-----PNSDST---LNSRQLEPRTE 271
 DB 363 AFSFOEFLSLNSSPLDIRKKLSGLPRLDENSAEBGPWEDPGTGMWQGTGPTGSD 422
 QY 272 TDSVG-----TPQNGMRLHDPVSKTVIKPESC-----VPCGKRIK 309
 DB 423 VDSVGGSGESRSIDSPISPGAGTROLVKASSTGTSESSDDFEERDDLDGLDNLGSGSPF 482

QY 310 GKLSL-----KCRDCK--VSHPECDR--RCPLPCIPTLI-----340
 DB 483 GKWTLSAQAQTHQLRRLRSPACRCECAFMVSGTECECFLTCHKRCLFTLLICGRRRL 542
 QY 341 --GTPKIGGML---ADFSQTSPIPSIVHCVNIEIQRGLTETGLYRISGCDRTVKE 395
 DB 543 PARTPL-FGVDFQLPRDPEE---VPFVVTCTAIEIHRALDVQGIYRVSGRVRYER 597
 QY 396 LKEKFLRVKTVPLLSKYDDIHAICSLIKDPLRNKEPULTFRLNRAFMEEAETDEBD---452
 DB 598 LQCAFENGALVBLSG-NSPHVSSVLKRFLOELTEFPVLFPHLYDAFISLAKTLHDPGD 656
 QY 453 -----NSIAAMTQAVGELPQANRDTLALMTLQRY-AQSPTKQDVANLAVFGP 502
 DB 657 DPGTPSPSPDVIRSLKTLIVQLPDSNYNTLRLHLVAHLFRVAARFMENKASANNLGIIVFGP 716
 QY 503 TIYAHAVPRPD-----PYMSQDIKXQPKVVEHLLSLPLEYWSQPMWVEQENIDPLH 554
 DB 717 TLIR---PPDGPRAASALPVTCLLDSGHQAOQV-----PLIVHYEQLFQMD 760
 QY 555 VIENSNAFSTPQTPDIKVLGFPVT-----PEHQ---LTKTPS-----SSSLSQ 596
 DB 761 ELRPQ---ATEPPQDPSPAPRGELTSSQRPPEHLPDQRPVLAADPGDPQGHSTLBO 816
 QY 597 RVRSTLTK-NTPRFGSKSKATN-----LGRQ--GNFPASP 629
 DB 817 HPTATPTETPTQSDQREDAEDTKDGGGEVSSQGPEDSLGTQSRGHFSRCP 869

Search completed: February 1, 2005, 14:20:01
 Job time : 57 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 1, 2005, 14:09:12 ; Search time 40 Seconds
(Without alignments)
1047.824 Million cell updates/sec

Title: US-09-881-736a-2

Perfect score: 3243
Sequence: 1 MPTMLNVLNLEPQLVRVE.....SKSATNLGRGNFPASPMLK 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	9.3	1261	3	US-09-080-855-2
2	301	9.3	1261	4	US-09-566-076-2
3	270.5	8.3	2548	3	US-09-172-422-1
4	257.5	7.9	165	5	PCT-US93-03076-10
5	230	7.1	140	5	PCT-US93-03076-9
6	214.5	6.6	547	4	US-09-855-323-15
7	210	6.5	1513	5	PCT-US93-03076-2
8	202.5	6.2	946	4	US-09-538-092-1230
9	200.5	6.2	1702	4	US-09-854-133-434
10	198.5	6.1	645	4	US-10-164-595-40
11	197.5	6.0	638	4	US-10-164-595-73
12	195.5	6.0	537	4	US-09-270-767-32573
13	195.5	6.0	537	4	US-09-270-767-47790
14	192	5.9	333	4	US-09-507-765-32
15	192	5.9	433	4	US-09-507-765-31
16	191	5.9	433	4	US-09-507-765-31
17	191	5.9	2071	4	US-09-415-522-6
18	188.5	5.8	439	4	US-09-507-765-33
19	186	5.7	159	4	US-09-248-796A-14549
20	183.5	5.7	162	5	PCT-US93-03076-8
21	179.5	5.5	581	4	US-09-270-767-33206
22	179.5	5.5	581	4	US-09-270-767-48423
23	172	5.3	362	4	US-09-270-767-41652
24	169.5	5.2	1007	4	US-09-538-092-736
25	161	5.0	1013	3	US-09-415-522-8
26	151	4.7	282	4	US-09-248-796A-20596
27	150.5	4.6	197	4	US-09-270-767-33381

28	150.5	4.6	197	4	US-09-270-767-48598	Sequence 48598, A
29	150.5	4.6	216	4	US-09-513-999C-5155	Sequence 5155, Ap
30	146	4.5	274	4	US-09-248-796A-20527	Sequence 20527, A
31	146	4.5	304	4	US-09-248-796A-20526	Sequence 20526, A
32	140.5	4.3	567	4	US-09-270-767-33051	Sequence 33051, A
33	140.5	4.3	567	4	US-09-270-767-48268	Sequence 48268, A
34	139	4.3	422	4	US-09-248-796A-14141	Sequence 14141, A
35	138	4.3	162	4	US-09-270-767-33895	Sequence 33895, A
36	138	4.3	387	4	US-09-248-796A-20549	Sequence 20549, A
37	133	4.1	724	4	US-09-621-976-7641	Sequence 7641, Ap
38	131.5	4.1	119	4	US-10-138-701-24	Sequence 24, Appl
39	130.5	4.0	667	4	US-09-538-092-1102	Sequence 1102, Ap
40	129	4.0	1505	4	US-09-735-934A-2	Sequence 2, Appl1
41	128.5	4.0	878	3	US-10-060-332-2	Sequence 2, Appl1
42	128.5	4.0	878	4	US-10-339-657-2	Sequence 2, Appl1
43	127.5	3.9	204	4	US-09-270-767-56893	Sequence 56893, A
44	127.5	3.9	1354	3	US-08-685-871-2	Sequence 2, Appl1
45	127.5	3.9	1354	3	US-08-685-871-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-09-080-855-2
; Sequence 2, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Sataa, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Hejld, Carl-Henrik
; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-2

Query Match          9.3%; Score 301; DB 3; Length 1261;
Best Local Similarity 22.4%; Pred. No. 7.9e-19;
Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;

QY 9 RNLEPQLVRVEVLSCNEVOFQLAKDPEDPRKKQKQFDHE LGKYKULMAKTERSA 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 372 RLREBALQKVE---EADELYKV-CVTNVEERNDVENTKRETLAQLTLVPCDULLKA 427

QY 68 LDVFLKHANNOVDVETKROBAEADCEKLERQQLIREMLMCDTSGSISLUSEBOK---SA 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 428 VTNLNLHMGHLQAASLADRLQSLCGSAKLYDEQGESEFVKATNS-----TEBEKVDGNV 482

QY 125 LAFNLNGOPSSNAGNKRLLSTI---DESGIISLDSIFDKTDESLWDSSLVKTKLKKE 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 483 NKLHNSQPSGFGFPANSLSDVVRLLPSSNKKIEEDRCSNADIT---GPFIRWTFGWMS 539

QY 182 KRSTSRQVVDGPPGVKTRSGSAVVDGNSIYAKTTVYPNDGPIEAVSTIETVY 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 540 DSEST-----GGSSSSRSIDS-----BSI-----SGPD----- 562

QY 242 WTRSRKKTGLPWNNDSTLNSKOLEPRTET---DSVGTPOS---NGAMRLHDFVSKTVIK 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 563 FHKFLPRTSSGMSADLDDEHEPSPSEITGNSLGTIKKTLMSKALATHKF--RKLS 620

QY 297 PESCVPCGRKIKFGKLSLKCRCRCRVVSHPECRCPLPC---IP---TLIGTVKIGB 349
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Db      621 PTKCDEGIVF--QGVCECECLVCHKCKLENIYICGHOKLPCKIHLFG----- 670
Qy      350 MLADF--VSQTSR-MIPSIYVHCNEIEORGLTETGLYRISGCDRTVXELKEKFLRVKT 406
Db      671 --AEFTLVAKKRPDGIPIFLKICASEIENRALCIGIYVCG-----NKIKTE 716
Qy      407 PLSKYD-----DI-----HAICSLKDFLNKKEPLLTPRLNAPMEAE-----ITDE 451
Db      717 KLCIALENGMHLVDISEFSSHDICDVLKYLRLQPEPFLFLYKEFIDLAKIEIGHVNE 776
Qy      452 DNS-----IAMYAVGELPOANDTLAFIMIHQRYA--QSPHTK 490
Db      777 QETKNSLEDKKMPNKCIEINRILKSKDLRLQPLASNPNLSHFLIVHLKRVVDIAEENK 836
Qy      491 MDVANIAKVFPTTIVAAVNPND--PVTMSQ--DIKQPKVERLLSLPLEYWSQFM--- 543
Db      837 MNSKULGVIFGFSILR---PRQTAPIITISLAEYNOARLVEFLIT-----YSQKIFDG 888
Qy      544 -MVEQENIDPLAVIENS--NAFTPTQPDIKVSLIGPVTTPBHQLKTPSSSSLSQRYR 599
Db      889 SIQPDVWMSIGVVOGCEPCKPLSPBERDIERSMKSLFFSSKEDIHTSESSEKIFERAT 948
Qy      600 STLTKNTPRFGSKSATNLGR 621
Db      949 S-----FESEKQNALGK 962
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RESULT 2
US-09-566-076-2
; Sequence 2, Application US/09566076
; Patent No. 6475775
; GENERAL INFORMATION:
; APPLICANT: Saratz, Jan
; APPLICANT: Pranzu, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Helman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heidlin, Carl-Henrik
; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPPL
; FILE REFERENCE: I0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; CURRENT FILING DATE:
; EARLIER APPLICATION NUMBER: 09/080,855
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-566-076-2
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Query Match 9.3%; Score 301; DB 4; Length 1261;

Best Local Similarity 22.4%; Pred. No. 7.9e-19; Matches 153; Conservative 120; Mismatches 249; Indels 160; Gaps 33;

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Qy      9 RNILFQOLYARVVEILSEGEVQFIQAKDFEDFRKKQRTDHE-IGKYDILMKAEATERGA 67
Db      372 RLLEBAALQKVE---EADLLYKV-CYTNVEERRNDVENTKREILAQRLTLVQCDLITLKA 427
Qy      68 LDVYKLKHAHQVDEIKRQRAADCEKLERQIQLIREMIMCDTSGSISLSEQK---SA 124
Db      428 VTVNLFHMQLDAASLADRLQSLCSGAKLYDPQGEVSEFVKATNS-----TEBEKVGNV 482
Qy      125 LAFILRGQSSSNAGKRLSTI---DESGISLSDISFDKTDLSLMDSDSLVYTFKLAKKE 181
Db      483 NKLHNSQSGSGGPNASLSDVLRPLPSSNKIEEDRCNSADIT---GPSFIRSWTFGMS 539
Qy      182 KRSTSRQGVDPGPPGVKTRSIGSAVDQGNESIVAKTVTVPNNDGPIEAVSTIETVY 241
Db      540 DSEST-----GGSSSRSLDS-----ESI-----SPGD----- 562
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Qy      242 WTRSRKGTGLQPMNSDTLNSRQLEPRTT--DSVGTPOS---NGGRHLDPFSKTVIK 296
Db      563 FHRKLPRTTSSGTMSSADDEREPPSPSEBTGPNLGTFFKTLMSKALTHKF--RKLS 620
Qy      297 PESCVPCGRIRIKFGSLSKRCRQVSHPEGRCPPLC-----IP---TLIGTPVIGBG 349
Db      621 PTKCDEGIVF--QGVCECECLVCHKCKLENIYICGHOKLPCKIHLFG----- 670
Qy      350 MLADF--VSQTSR-MIPSIYVHCNEIEORGLTETGLYRISGCDRTVXELKEKFLRVKT 406
Db      671 --AEFTLVAKKRPDGIPIFLKICASEIENRALCIGIYVCG-----NKIKTE 716
Qy      407 PLSKYD-----DI-----HAICSLKDFLNKKEPLLTPRLNAPMEAE-----ITDE 451
Db      717 KLCIALENGMHLVDISEFSSHDICDVLKYLRLQPEPFLFLYKEFIDLAKIEIGHVNE 776
Qy      452 DNS-----IAMYAVGELPOANDTLAFIMIHQRYA--QSPHTK 490
Db      777 QETKNSLEDKKMPNKCIEINRILKSKDLRLQPLASNPNLSHFLIVHLKRVVDIAEENK 836
Qy      491 MDVANIAKVFPTTIVAAVNPND--PVTMSQ--DIKQPKVERLLSLPLEYWSQFM--- 543
Db      837 MNSKULGVIFGFSILR---PRQTAPIITISLAEYNOARLVEFLIT-----YSQKIFDG 888
Qy      544 -MVEQENIDPLAVIENS--NAFTPTQPDIKVSLIGPVTTPBHQLKTPSSSSLSQRYR 599
Db      889 SIQPDVWMSIGVVOGCEPCKPLSPBERDIERSMKSLFFSSKEDIHTSESSEKIFERAT 948
Qy      600 STLTKNTPRFGSKSATNLGR 621
Db      949 S-----FESEKQNALGK 962
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RESULT 3
US-09-172-422-1
; Sequence 1, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/172,422A
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2548
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-172-422-1
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Query Match 8.3%; Score 270.5; DB 3; Length 2548;

Best Local Similarity 24.4%; Pred. No. 2e-15; Matches 130; Conservative 75; Mismatches 203; Indels 125; Gaps 24;

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Qy      143 ISTIESGSIISDIFDKTDESILMDSDSLVYTFKLKKEKRSTSRQGVDPGPPGVKTR 202
Db      1864 LKSMDE--FLKKVN-DLDNDSKCDITLVDFVFKALKAEFRQN-----IFSFY 1908
Qy      203 SIGSAVDQGN-----ESIVAKTVTVPNNG---GPIEA-VSTIETVYVTRSR 247
Db      1909 SGALAMDQKSIKYDLYALFQDILEKTMRLQORDSLGESPVYVWVNTFKVYLDRYMNEF 1968
Qy      248 KTGTLQPMNSDSTL-----NSRQLEPRTTETSVGTPOGNGMKRLHDPFSKYVIRESCVY 302
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Db 1669 KT-----SDCTATVPTTERKRRKKTDLV--EHNH-----HIFKATQVSIPTCYC 2015
QY 303 CGKRIKFGKLSKCRDCAVSHPECHRCPLPCIPITLIGTPVIGE-----GMLADPV 355
Db 2016 CSSLIMIMBASVCKCKYACHKKC-----CLKTTAKCSKKYDELSSRQGVLSRL 2068
QY 356 SGTSPMIPSIIVHCVNEIFQRTGTEGLYRISGCDRTVKEKELRVKTVPLSKYVD- 414
Db 2069 TSEDRTVPLVEKLIVIEHGLYTEGIYKSGSTNIXELRQ---GLDPAESVNLDDY 2125
QY 415 -THATSLKDLPLRNKEPLTFRLNRAFMEEAETIDEDNSIAAMYQAVGELPQANDTL 473
Db 2126 NTHVIAVSFKQWRDLPNPLMTFELYEEFLRANGLDERKETIGVSVLDQSLRTHLNL 2185
QY 474 AFIMIHQVVA--QSPHTKMDVANLAKVFGPTIVAHAVPNPDPTWMSQDIKROPKVERLL 532
Db 2186 ERLIFLTVRIALQEDNTRMSANLAIYFAPCIL-RCPDPTDPLQSQVODISKTTCE--- 2241
QY 533 SLPLEYWSQFMWYEQN-----IDPLHVIENSNAFSTPQTPDIKVSLL----- 575
Db 2242 -----LIVEQNNKYARKLDISLFEAKN-----AKTRLSLIRSMGKGR 2284
QY 576 -----GPVTPPHQLKTPSSSLSGQVRSITLTXTPRGSKSKATNLGRQ 622
Db 2285 RRGNYRGP-SSP--VVVRLPVSVDVSE--ETLT-----SEAMETDITEQ 2324
RESULT 4
PCT-US93-03076-10
Sequence 10, Application PC/TUS9303076
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
TITLE OF INVENTION: GAP-Associated Protein p190 and
TITLE OF INVENTION: Transduction
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03076
FILING DATE: 19930331
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI92-03A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-03076-10
Query Match 7.9%; Score 257.5; DB 5; Length 165;
Best Local Similarity 37.9%; Pred. No. 3,4e-16;
Matches 64; Conservative 33; Mismatches 63; Indels 9; Gaps 4;
QY 369 CVAIEIQRGLTETGLYRISGCDRTVKEKELR-VKTVPLLSKVDIDHAIKSLKDFL 426
Db 1 CIREIEBGRGLNSBGLYVSGFSDLIEDVKNAFDRDGEKADISVMYEDINITGALKLYF 60

QY 427 RNKEPDLTFRLNRAFMEEAETIDEDNSIAAMYQAVGELPQANDTLAFLMIHLQVAA 486
Db 61 RDLPIPLITYDYAPKXIEBSAKIMDPDEQLETHBAKLLPAPACETLRIMATLKV--T 118
QY 487 PHTK---MDVANLAKVFGPTIVAHAVPNPDPTWMSQDIKROPKVERLL 532
Db 119 LHEKENLMAENIGVFGPTLMRS--PELDMAALNDIRYQRLVELLI 165
RESULT 5
PCT-US93-03076-9
Sequence 9, Application PC/TUS9303076
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
TITLE OF INVENTION: GAP-Associated Protein p190 and
TITLE OF INVENTION: Transduction
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03076
FILING DATE: 19930331
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI92-03A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-03076-9
Query Match 7.1%; Score 230; DB 5; Length 140;
Best Local Similarity 38.8%; Pred. No. 1.1e-13;
Matches 54; Conservative 24; Mismatches 59; Indels 2; Gaps 2;
QY 369 CVAIEIQRGLTETGLYRISGCDRTVKEKELR-VKTVPLLSKVDIDHAIKSLKDFL 427
Db 1 CVEIEIRRGMEVGIYRVSQVATDIOALKAFVNNKDVSVMSQMDVNLACTLKYFR 60
QY 428 NKEPDLTFRLNRAFMEEAETIDEDNSIAAMYQAVGELPQANDTLAFLMIHLQVAA 487
Db 61 ELPEPLTFDEYFNPFBEGIALSDPAKESCMNLNLSPRANLTLFLDLHLKRVAKKE 120
QY 488 H-TKMDVANLAKVFGPTIV 505
Db 121 AVNKMGLHNLATVFGPTLL 139
RESULT 6
US-09-855-323-15
Sequence 15, Application US/09855323
Patent No. 6602667
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmutz, Wayne

```

/ APPLICANT: Klingler, Tod M.
/ TITLE OF INVENTION: Inflammation-Associated Polynucleotides
/ FILE REFERENCE: PB-0006-1 CIP
/ CURRENT APPLICATION NUMBER: US/09/855,323
/ CURRENT FILING DATE: 2001-05-14
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PERL Program
/ SEQ ID NO 15
/ LENGTH: 547
/ TYPE: PR1
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: 2471716CD1
US-09-855-323-15

Query Match          6.6%; Score 214.5; DB 4; Length 547;
Best Local Similarity 29.2%; Pred. No. 36-11; 75; Indels 29; Gaps 3
Matches 57; Conservative 34; Mismatches 389

QY      349  GMLADFY-----SQTSPMIPSIIVHCVNEIEQGLTETGLYRISGCDRTVKELKEK 399
Db      330  GLRDQVGGCOLSELCQREGDTPSFLRLCIAAVDKRGDVGIVRSGNLAVVQKLRFL 389
QY      400  FLKXKTVPL-----LSKVDIHAIQSLKDPFLRNKEPILTRLR 440
Db      390  VDREAIVTSDGRYVPEPQGGEGRLDLDSTEMDDIHVVGALKLFLRELPLQVLP 449
QY      441  AFMEAETTEDNSIAMIYQAVGELPQANRDTLAFIMILQGV-AQSPHTKMDVANIAYK 499
Db      450  HFRALALASESGQCSQIQELGSMKPRHDTLRYLREHLGVIAHSDKNRMTPHNLGIV 509
QY      500  FGPITVAHAVPNEDP 514
Db      510  FGPTLFRPEQETSDP 524

RESULT 7
PCT-US93-03076-2
/ Sequence 2, Application PC/TUS9303076
/ GENERAL INFORMATION:
/ APPLICANT: Whitehead Institute for Biomedical Research
/ TITLE OF INVENTION: GAP-Associated Protein p190 and
/ TITLE OF INVENTION: Transduction
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
/ STREET: 2 Militia Drive
/ CITY: Lexington
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/03076
/ FILING DATE: 19930331
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Graham, Patricia
/ REGISTRATION NUMBER: 32,227
/ REFERENCE/DOCKET NUMBER: WHI92-03A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1513 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein

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[illegible]

NAME/KEY: misc_feature
 LOCATION: (0)...(0)
 OTHER INFORMATION: Polypeptide Accession Number P98171
 US-09-538-092-1230

Query Match
 Best Local Similarity 21.4%; Score 202.5; DB 4; Length 946;
 Best Local Similarity 99; Mismatches 256; Indels 170; Gaps 27;

45 QRTDH---ELG---KYKDLIMKAFTERSLADVKLKHARNOVVEIKRRQRAADECKLE 97
 130 QRSIHAEDVGRVYKSRDLQDLLEVSELQAKTYQAYHNEVNAERKUREAL 189
 98 RQIQ-LIRELMCDTSGSIQISEOKSAL-----AFINRGQSSSNANKRLST 145
 190 ROEKRAAGSVPTTGATAGPLRKSSLKGGRLVEKRAKMEHLKCTKARNEVLLS 249
 146 IDBSGSLSDISDKTDESIDMDSLVKTFKLKREKRSTSRQVDPGPGVKTRSIG 205
 250 L--ASVNAVASNYVYLDVLDLMDCCDTGPHLALGVLRSTYTAESRTQASQVQGLSLE 306
 206 SAVD---QGNESIVAKTIVT-----PNDGPIEAV----- 233
 307 EAVEALDPEDKAKVLEHATVFCPLRPDYHPHDGVEAIECEVELKDELIPRAQNIQ 366
 234 ----STIETVPWTSRRKKTGLQPW-----NSDSTLNSRLQLEPTETDSVGTPOSG 282
 367 SRLDRGTITEEV--NKTILKATLQALLBVASDDGDVLDSPQTSPTT--SLKTSISDP 421
 283 GNR-----LHDFVSKTVIKPESCVPCGKRIKRGKLSLK----- 315
 422 GSRQAGRRRGQOQETETFYLTQLQEYLS-----GRSI-LAKLOAKHEKLOEAL 468
 316 ---CROCRVVSHEC-----RDRCPPLCT--PTLIGTPVKIGEGMLADPVQSPTMIP 363
 469 QRGDKKEQESWTQYQRFQKSRQPPSSQYNORLFG-----GMEXFIQSSGQVPV 521
 364 SIYVHCVNEIEQRLTETGLYRISGCDRTVKELEKEFLRKVYVLLS--KYDDIHAICSL 421
 522 LVESGIRFINLNGLOHEGIFRVSQAOARSEIRDAFERED-PLVGGCAHLDSDVAGV 580
 422 LKDFLNLEKPELLTRLNRAFMBAETDEDSIAAMYQAVGELPQANRDTLAFIMIHQ 481
 581 LKLYFRSLRPPPLPPLPFGELLASSELDETAERHEVSRLLMLRPAVLVLAFLYLFTEFN 640
 482 RVAQ--SPHTKMDVANLAKVGFPIVAHAVNPDPVMSQDIKQPKVVEELLSPLEYS 540
 641 HLAQYSDENMMDYNLAVCFGPILL-----FVPAGDPPVALQGRVNLV----- 684
 541 QFMVVEQENIDPLHVIENSNAFSTPQTPDIKVISLGLPVTTPHQLEKTPSSSSLSQ-RVR 599
 685 QTLIVPDRVFP-----PLT-----SLPGFV--YKCAAPFASCLGDAQLE 724
 600 STLTKNTP 607
 725 SLGADNDP 732

RESULT 9
 US-09-854-133-434
 Sequence 434, Application US/09854133
 Patent No. 6759508
 GENERAL INFORMATION:
 APPLICANT: Lodes, Michael J.
 APPLICANT: Mohamath, Raedon
 APPLICANT: Henderson, Robert A.
 APPLICANT: Benson, Darin R.
 APPLICANT: Secrist, Heather
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 FILE REFERENCE: 210121.475C10
 CURRENT APPLICATION NUMBER: US/09/854.133
 CURRENT FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 735
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 434
 LENGTH: 1702
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-854-133-434

Query Match
 Best Local Similarity 28.3%; Score 200.5; DB 4; Length 1702;
 Best Local Similarity 94; Mismatches 95; Indels 33; Gaps 12;
 Matches 72; Conservative 54;

364 SIYVHCVNEIEQRLTETGLYRISGCDRTVKELEKEFLRKVYVLLS---VDIHAICS 420
 2 AVLGSCAFIERGIYD-GYRLSGVASNIGRLRHF-DSEHVPDLTKERYVDHSVGS 59
 421 LKDFLNLEKPELLTRLNRAFMBAETDEDSIAAMYQAVGELPQANRDTLAFIMIHQ 480
 60 LCKLYFRSLRPPPLPPLPFGELLASSELDETAERHEVSRLLMLRPAVLVLAFLYLFTEFN 119
 481 QVVAQ--SPHTKMDVANLAKVGFPI-----VAHAVNPDPVMSQDIKQPKVVERLLS- 533
 120 SLADYCSITNMHAKALVAMBNLRSKOIESACFSGRARF--EVRIQSVVVERPLNH 177
 534 LPLEWSQPMVVEQENIDPLHVIENSNAFSTPQTPDIKVISLGLPVTTPHQLEKTPSSSS 593
 178 VDLVFGSRISMAWQ-----EGAASLSRPK-----SLT--VASPTKLTLEBAQA 220
 594 LSG-RVRSITL-TKN 605
 221 RTQAVNSPVTEN 234

RESULT 10
 US-10-164-595-40
 Sequence 40, Application US/10164595
 Patent No. 6657054
 GENERAL INFORMATION:
 APPLICANT: Origene Technologies, Inc
 TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
 FILE REFERENCE: IU 103 R1
 CURRENT FILING DATE: 2002-06-10
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 40
 LENGTH: 645
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-164-595-40

Query Match
 Best Local Similarity 20.2%; Score 198.5; DB 4; Length 645;
 Best Local Similarity 77; Mismatches 174; Indels 129; Gaps 18;
 Matches 96; Conservative 77;

166 DMDSLVKTFKLKREKRSTSRQVDPGPGVKTRSIGSAVDQGNESIVAKTIVTPN 225
 8 NMD-----FNLKVEAKIARSRVMTG-----EQMAAHFSPSTPN 42
 226 DGGPIEAVSTIETVPWTSRRKKTGLQPNWSDSTLNSQLERTETDSVGTPOSGNMR 285
 43 ---PLERPIKMG--WLKKQR--SIVKW-----QQRVFLVRAQ-----Q 74
 286 LHDVFSKTVIKPESCVPC-GKRIKPKLSLKCDKCVVHPERDRCPLPIPT----- 338
 75 LYYKDEBDTKPQGCWYLDPGCTIK-----BIANPEAGFVEEIIIPASWDQNR 123
 339 -----LIGTPVKIGEGMLADPVQSOTSP-----MPSIVVHC 369
 124 MGDSYVLAASSQAEMEWKFLRRVAGTFCGFGRLBETAVAYEKGFGHVLPIVENC 183
 370 VNEIEQRLTETGLYRISGCDRTVKELEKEFLRKVYVLLSKVDIHAICSLKDLFLNLT 429

```

Db      184  AEFILHEGRNEGRIPLRLPQDNLVYQLRDAF--DAGERPSEFDRTDVTGHVTAASLLKLYRLDL 242

QY      430  KEPILTFPLNRAFMETAETTEDBNSTIA--AMTQAVGEELPQANKDTLAFMLTHIQRY-AQS 486
        :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      243  PEPVPMQSYEGFLLCGQLTNDADKAAQOELMKQSLTLEPRDNYSLSYICRFHEHIQLNC 3020
        :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

QY      487  PHTKMDVNLAKVPEGPTVAHVAPNDPVTMSQDILRQCKVYVERLLSLPLEYWSQPMVE 546
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      303  AVNKKSVNLAIVIGNLIRSKVEBP-----AVIMRGTPQIQIRVMT-----MMIR 347

QY      547  QENI-----DPLHYIENSNAFSPQTEBDIKVSLGLPATTPEHOLKTPSPSSSL 595
        :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db      348  DHEVLPFKSKDIPLESPPAQK---DPKKAIPVARSISGMATEDLRIKSRIDSESMAT 400

```

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RESULT 11
US-10-164-595-73
; Sequence 73, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: 1U 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-595-73

```

Query Match	6.1%;	Score 197.5;	DB 4;	Length 638;
Best Local Similarity	24.5%;	Pred. No. 1.6e-09;		
Matches 66;	Conservative 53;	Mismatches 117;	Indels 33;	Gaps 8

```

Oy      341  GPVYVIGEGMADFPVSQTSR-----MPSVYVHVNVNIEORGLETGTGLYRSGCDRTYKEL 396
Db      144  GTPCGVFPQGRUDEYTAAYEOKFGEPHVLPILVEKCAEPILEGRNBBGI FRLPQGDNLVYKOL 203
Oy      397  KEKPLRVKTVPLLSKVDIDHAI CSLIKDPLRLNKEPLLTFRLNRAFMEEAETDEDSIA 456
Db      204  RDAF--DAGRRPFPDDTDVHTVASTLIKTLRLDPEEVVWPSQYEGFLLCQLTNADAEAKA 262
Oy      457  --AMVQAVGELQOARBDTLAFIMHIGRY-AQSPHTKMDVANKYEGPTVAHAVNPD 513
Db      263  QOELMKQSLIRPDNTSLSYICRFHEHITQLNCAVNMKSVNDLAIYIGVNLISKYEDP- 321
Oy      514  PVTMSQDILKQKQVVERLLSLPLEYWSQEMMVEQENI-----DPLVHTIENSNAFSTPQ 566
Db      322  ----AVIMRGTPQIQRVWMT-----MMIRDHEVLFPKSKDQIPLSPQAQKN---DPK 364
Oy      567  TPDIKVSLLGPVTPTEPHQILKTPRSSSLSS 595
Db      365  KAPVARSVSVMGDATEDLIRISRTDSFSSMT 393

```

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RESULT 12 767-32573
; US-09-270-767-32573
; Sequence 32573, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-034
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32573
; LENGTH: 537
; TYPE: PRT
;

```

ORGANISM: *Drosophila melanogaster*
US-09-270-767-32573

Query Match	6.0%;	Score 195.5;	DB 4;	Length 537;
Best Local Similarity	22.5%;	Pred. No. 1.9e-09;		
Matches 92;	Conservative 66;	Mismatches 172;	Indels 79;	Gaps 17;

258 D S T L N S R O L E P R E T T D S V G T P O S G K G M R L H D F V S K T V I P E S ----- C Y P G K R 306
 128 D S E T N T A V I A V S N T S I D V C S S N S S G G ----- S P A V G S K S G C D D R N G L E C C S S C S K R 180

QY 307--ATKFGSLKCDRCRVTS---HPECIDRCPCIPITIGTPVKI-----SEGMLAD 353

Db 181 HDLKQRMHTLE-ODLLVQTTYSQELQKQSCP-TLAFGGDEBPVLVQEOETQGRNRCGNS 238

QY 354 FVVGQTS-----MIPSIWCHVNEIENGGLTET---GLYRISGCDRTV 393

Db 239 ASSSTKPCFDTELEMLVKHDHRTVPRIIVDCDLIQKQYRRSTQPIEGYRQCCDYNKI 298

```

QY      394 KELKEKFLRVKTPPLLSKYD-DTHAICSLDKDFRLNKEPPLTFRLRNFRMEAAE---IT 449
Db      299 QTLRFSS-IDANDYDLSLRQPDVDLHTLTGLKLFREIKSPLVRVNEAKFTIGQPNQMLLT 357

```

DQ
Y

450 DEDNSIAAMYQANGELPOANRDTLAFIMTHLORAQSPTHKMDVLANAKFEGPTVAHAV 509

DB
Y

358 DLISAKLDRLKRSLPESNRDMWDYIEGHFNRRITTKVLPCQLISAETLSISTVPSPLE-HTV 416

QY 510 PNEDPVTMSQDIKQPKVVERLISLPLEWSQFM--MVGQENIDPLHVI---ENSNAST 564

Db 417 PGQGHMODIOLIREGETTLADCVYLMIEGRIIDRLRHPNRSPTWAVVANGSNPLRN 476

QY PQPPDIK---VSLIGPVTT-----PEHOLTKPSSSSISQRV 598
| : | : | : | : | : | :
DH PETPSTRKETPOLIVPLATTSYYENSPNRPYPKWFSKIPGSTRTRYI 525

```

RESULT 13
US-09-270-767-47790
; Sequence 47790, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47790
; LENGTH: 537
; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-270-767-47790

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Query Match	6.0%;	Score 195.5;	DB 4;	Length 537;
Best Local Similarity	22.5%;	Pred. No. 1.9e-09;		
Matches 92;	Conservative 66;	Mismatches 172;	Indels 79;	Gaps 17

```

QY      258  !STLNSRLQERTENDSVGTQPSQNGKMLAHFVSTVJVKPES-----CVPCGKR- 306
Db      128  DDSNTAVLVNTSITDVCSSNSSSG-----SPAVGRSKSGRRRRNGLECCSSCSKRW 180

QY      307  --IKFGKSLKRCDCRVVS---HPECRDRCPPLCPIPLTGPYKI-----GEGMLAD 353
Db      181  HDLQGRMHTE-QDLVQVTTYSGELEGSGCP-TLAPGGLBEPVLEQGTQGRNRCGS 238

QY      354  FVSGTSP-----MIPSLVHCVNEIQRGLTE---GLHISGCDRV 393
Db      239  ASSSTKPCPDETELEMLKHDQRRTPRIVDCCDLIEQKRRSTQPIBIGIYQCCDYNKI 298

QY      394  KKLKELPRVKTVPFLSKVD-DIHAICGLLDPLRNKLEPLLTFPLNKAFFMAAE---IT 449
Db      299  QTLRFPS-IDANDYSLRQPDVHILTVGLKFLPKEISPLRVNEAETFGIQPNOMILT 357

```



```

QY      450 DEBNIAAMYQAVGELPOANDRTLAFLMIHLOEVAOSPHTKMDVANLAKVGPPIVAHAV 509
      358 DLSAKDLSKRLRLRSIPESNRDTMDYIFGHFNRLITKVLQOIAEELTSSVTSIF-HIV 416
DB
QY      510 PNPDPVTMSQDIKQKQKVVVERLLSLPLEYWSQFM--MVEQENIDPLHVI---ENSAVST 564
      417 POGVHMDIQQLLREGETLADCVKMIEXGRIFDRLRPHRPSPTMAVAVANGSGNPLRN 476
DB
QY      565 PGPDPK--VSLGPGVT-----PEHQLKTPSSSSLSQSV 598
      477 PEIPSTRKETPOLVPLATTISYPNSPNRKYPSWSKIPGSIHRTYRI 525
DB

```

RESULT 14

```

US-09-507-765-32
; Sequence 32, Application US/09507765
; Patent No. 6509155
; GENERAL INFORMATION:
; APPLICANT: Klingner, Tod M.
; APPLICANT: Stewart, Elizabeth A.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS
; FILE REFERENCE: PC-0010 US
; CURRENT APPLICATION NUMBER: US/09/507,765
; CURRENT FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6509155 96572185
US-09-507-765-32

```

Query Match

```

Best Local Similarity 26.6%; Score 192; DB 4; Length 333;
Matches 78; Conservative 46; Mismatches 109; Indels 60; Gaps 12;

```

```

QY      325 PEGRDRCPICPIPT-LIGTPVKIGEGMLADPVSQTSPIVHCVNEIBORGLETGTG 383
      77 PPTKTPPPRPPLPTQOFGVSLQ---YKLD--KNQGEIIPVLRFTVYLRKGLRTEGL 130
DB
QY      384 YRISGCDRTVKELKEKFLAVKTVPLLSKYDDIHAICSLKDFLRNKEPLLTRLRATM 443
      131 FRRSASVQTVREIQRLYNQKPVN-FDDYGDIIIPAVILKTFLRELPOPLTF---QAYE 186
DB
QY      444 EAAETDEDNS--IAAMYQAVGELPOANDRTLAFLMIHLOEVA-OSPHTKMDVANLAKVF 500
      187 QILGITCVSSSLRVTCGQILRLSLPEHNYVLRKLMGFLHANSRESIFNKMSSNLACVF 246
DB
QY      501 GPTIVAHAVNPDPVTMSQDIKQKQKVVVERLLSLPLEYWSQFMVVEQENIDPLHVIENS 560
      247 GNLN-----IMPSQGVSSLSLV-----PLNMFTELLIEYEKI----- 280
DB
QY      561 APTSTPTPIKVSLLGPVTTPEHQL-----KTPSSSSLSQSVSTLTXT 606
      281 -FSTPEAPG-----EHGLAPWEGSGRAAPLOEAVPRTQATGLTKPT 320
DB

```

RESULT 15

```

US-09-507-765-30
; Sequence 30, Application US/09507765
; Patent No. 6509155
; GENERAL INFORMATION:
; APPLICANT: Klingner, Tod M.
; APPLICANT: Stewart, Elizabeth A.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: GTPASE ACTIVATING PROTEINS

```

```

; FILE REFERENCE: PC-0010 US
; CURRENT APPLICATION NUMBER: US/09/507,765
; CURRENT FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6509155 3068538CD1
US-09-507-765-30

```

Query Match

```

Best Local Similarity 26.6%; Score 192; DB 4; Length 433;
Matches 78; Conservative 46; Mismatches 109; Indels 60; Gaps 12;

```

```

QY      325 PEGRDRCPICPIPT-LIGTPVKIGEGMLADPVSQTSPIVHCVNEIBORGLETGTG 383
      177 PPTKTPPPRPPLPTQOFGVSLQ---YKLD--KNQGEIIPVLRFTVYLRKGLRTEGL 230
DB
QY      384 YRISGCDRTVKELKEKFLAVKTVPLLSKYDDIHAICSLKDFLRNKEPLLTRLRATM 443
      231 FRRSASVQTVREIQRLYNQKPVN-FDDYGDIIIPAVILKTFLRELPOPLTF---QAYE 286
DB
QY      444 EAAETDEDNS--IAAMYQAVGELPOANDRTLAFLMIHLOEVA-OSPHTKMDVANLAKVF 500
      287 QILGITCVSSSLRVTCGQILRLSLPEHNYVLRKLMGFLHANSRESIFNKMSSNLACVF 346
DB
QY      501 GPTIVAHAVNPDPVTMSQDIKQKQKVVVERLLSLPLEYWSQFMVVEQENIDPLHVIENS 560
      347 GNLN-----IMPSQGVSSLSLV-----PLNMFTELLIEYEKI----- 380
DB
QY      561 APTSTPTPIKVSLLGPVTTPEHQL-----KTPSSSSLSQSVSTLTXT 606
      381 -FSTPEAPG-----EHGLAPWEGSGRAAPLOEAVPRTQATGLTKPT 420
DB

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Search completed: February 1, 2005, 14:20:36
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: February 1, 2005, 13:57:16 ; Search time 202 Seconds

(without alignments)
1800.182 Million cell updates/sec

Title: US-09-881-736A-2

Perfect score: 3243
Sequence: 1 MDITMLNVNLFQQLVRRVE.....SKSATNLGRQGNFFASPMUK 632

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_02:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3243	100.0	632	2	Q9P2W2
2	3237	99.8	632	2	Q9H0H5
3	3230	99.6	632	2	Q9NMN2
4	2919	90.0	632	2	Q9P2S0
5	2781	85.8	628	2	Q9BZ74
6	2734	84.3	628	2	Q9WVW1
7	2497.5	77.0	629	2	Q6NRH9
8	2476.5	76.4	629	2	AAH70771
9	2476.5	76.4	629	2	Q6NVL1
10	2476.5	76.4	629	2	AAH67994
11	2462.5	75.9	629	2	Q7ZW66
12	2173	67.0	654	2	Q6P3H8
13	2173	67.0	654	2	AAH63983
14	1205.5	37.2	612	2	Q6DF11
15	1182	36.4	625	2	Q9H9L9
16	864	26.6	625	2	Q9H9L9
17	862	26.6	625	2	Q9H9L9
18	853	26.3	171	2	Q6P266
19	853	26.3	171	2	AAH24144
20	763.5	23.5	674	2	Q7PMW7
21	571.5	17.6	456	2	Q8MRH0
22	547.5	16.9	681	2	Q9XUS9
23	477	14.7	384	1	RG84_DROME
24	477	14.7	384	1	AAH68049
25	431	13.3	354	2	Q9SVR1
26	348	10.7	1980	1	MY9B_RAT
27	339.5	10.5	459	2	Q7ZU76
28	339.5	10.5	2114	1	MY9B_MOUSE
29	336	10.4	459	2	Q7T0E5
30	329	10.1	334	1	CHIN_RAT
31	328	10.1	334	1	CHIN_MOUSE

32	328	10.1	334	2	BAC35853
33	327	10.1	334	2	Q8BWU6
34	326	10.1	1107	2	Q6DE55
35	323.5	10.0	2158	1	MY9B_HUMAN
36	322	9.9	289	2	Q61BE0
37	322	9.9	289	2	CAG33145
38	322	9.9	459	1	CHIN_HUMAN
39	320	9.9	299	2	Q92153
40	315	9.7	1337	2	Q6PCS4
41	315	9.7	1337	2	AAH59184
42	310	9.6	459	2	Q7T0N5
43	308	9.5	635	2	Q94466
44	305.5	9.4	1317	1	GAP_CAEEL
45	303.5	9.4	332	2	Q6GN15

ALIGNMENTS

RESULT 1	Q9P2W2	PRELIMINARY;	PRT;	632 AA.
ID	Q9P2W2			
AC	Q9P2W2			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	GTPase activating protein.			
GN	Name=MgRacGAP;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI	TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20435340; PubMed=10979956;			
RA	Kawashima T., Hirose K., Satoh T., Kaneko A., Ikeda Y., Kaziro Y.,			
RT	"MgRacGAP is involved in the control of growth and differentiation of			
RT	hematopoietic cells."			
RL	Blood 96:2116-2124(2000).			
DR	EMBL; AB030251; BAA90247.1; -.			
DR	PIR; D59430; D59430.			
DR	HSSP; Q98935; 1F7C.			
DR	Intrac; Q9P2W2; -.			
DR	GO; GO:0005489; P:electron transporter activity; IEA.			
DR	GO; GO:0005506; P:electron transport; IEA.			
DR	GO; GO:0006118; P:electron transport; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.			
DR	InterPro; IPR002219; DAG_PE_bind.			
DR	InterPro; IPR000198; RhOGAP.			
DR	InterPro; IPR008936; Rho_GAP.			
DR	Pfam; PF00130; Cl_1; 1.			
DR	Pfam; PF00620; RhOGAP; 1.			
DR	PRINTS; PR00353; 4FE4SFDOXIN.			
DR	SMART; SM00109; Cl_1.			
DR	SMART; SM00324; RhOGAP; 1.			
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.			
DR	PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.			
DR	PROSITE; PS00238; RhOGAP; 1.			
DR	SEQUENCE 632 AA; 7100 MW; BC2B75E5A8739E2B CRC64;			
QY	Query Match	100.0%;	Score 3243;	DB 2; Length 632;
QY	Best Local Similarity	100.0%;	Pred. No. 1e-192;	
QY	Matches	632;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Db	1	MDITMLNVNLFQQLVRRVEILSEGNVOFIQAKDPEDFRKKMORTDHELGRYKDLWK 60		
Db	1	MDITMLNVNLFQQLVRRVEILSEGNVOFIQAKDFEDFRKKMORTDHELGRYKDLWK 60		
QY	61	AETERSALDYKLGKRNQVDVEIKRQRAADCEKLEKROLIQIRELMKCDTSSISLSEB 120		
Db	61	AETERSALDYKLGKRNQVDVEIKRQRAADCEKLEKROLIQIRELMKCDTSSISLSEB 120		

QY 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSGLVYTFKLKKR 180
DB 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSGLVYTFKLKKR 180
QY 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIAKTTVVPNDGPIEAVSTLETYP 240
DB 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIAKTTVVPNDGPIEAVSTLETYP 240
QY 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
DB 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
QY 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPPLCTPIITIGPVKIGEGMLADFVSQTSF 360
DB 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPPLCTPIITIGPVKIGEGMLADFVSQTSF 360
QY 361 MIPSIIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLKRVKTVPLLSKYDDIHAICS 420
DB 361 MIPSIIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLKRVKTVPLLSKYDDIHAICS 420
QY 421 LKDFLRLNKEPLTLFRLNRAFEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMLIHL 480
DB 421 LKDFLRLNKEPLTLFRLNRAFEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMLIHL 480
QY 481 QKVAOSPHTKMDVANIATAKFGPTIVAAVNPDPVTMSODIKRQKRVYERLLSLPLEYWS 540
DB 481 QKVAOSPHTKMDVANIATAKFGPTIVAAVNPDPVTMSODIKRQKRVYERLLSLPLEYWS 540
QY 541 QPMNVEQENIDPLHVTIENSNAPSTPOTPDIKVSLGCVTTPEHQLKTSSSSLSQRVSS 600
DB 541 QPMNVEQENIDPLHVTIENSNAPSTPOTPDIKVSLGCVTTPEHQLKTSSSSLSQRVSS 600
QY 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMUK 632
DB 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMUK 632
RESULT 2
Q9H0H5 PRELIMINARY; PRT; 632 AA.
AC Q9H0H5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp434C011 (RACGAP1 protein).
GN Name=DKFZp434C011; Synonyms=RACGAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Pousetka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Straubeberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136794; CAB6728.1; -;
DR EMBL; BC032754; AAH32754.1; -;
DR EMBL; CR533565; CAG38596.1; -;
DR HSSP; Q98935; 1F7C.
DR GeneW; HGNC:9604; RACGAP1.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR GO; GO:007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR000198; RhGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; CL_1; 1._GAP.
DR Pfam; PF06620; RhGAP; 1.
DR PRINTS; PR00353; 4FE4SFERDOXIN.
DR SMART; SM00109; CL; 1.
DR SMART; SM00324; RhGAP; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50238; RhGAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 632 AA; 71026 MW; 032B7DF9CEA8F39D CRC64;
Query Match 99.8%; Score 3237; DB 2; Length 632;
Best Local Similarity 99.8%; Pred. No. 2.4e-192;
Matches 611; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDTMNLNANLLEQOLVRRVEILSEGENVOFIQAKDFEDFRKKWORTHEICKYDLMK 60
DB 1 MDTMNLNANLLEQOLVRRVEILSEGENVOFIQAKDFEDFRKKWORTHEICKYDLMK 60
QY 61 AETESSALDVKLKHARNOVDVETIKRQRAEADCEKLERGIQLIREMLMCDTSGSIQLSSE 120
DB 61 AETESSALDVKLKHARNOVDVETIKRQRAEADCEKLERGIQLIREMLMCDTSGSIQLSSE 120
QY 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSGLVYTFKLKKR 180
DB 121 QKSALAFNLRGQSSSSNAGNKRSLSTIDSGSILSDISFPKTDBSLMDWSGLVYTFKLKKR 180
QY 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIAKTTVVPNDGPIEAVSTLETYP 240
DB 181 EKRRSTSRQFVDPGPPGVKKTSSIGSAVDQGNESIAKTTVVPNDGPIEAVSTLETYP 240
QY 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
DB 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTETDSVGTPOSGNGMRLHDFVSKTVIKPESC 300
QY 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPPLCTPIITIGPVKIGEGMLADFVSQTSF 360
DB 301 VPCGRIKRGKSLKCRDRCRVVSHPECRCRCPPLCTPIITIGPVKIGEGMLADFVSQTSF 360
QY 361 MIPSIIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLKRVKTVPLLSKYDDIHAICS 420
DB 361 MIPSIIVHCVNEIEQGLTETGLYRISGCDRTVKEIKERFLKRVKTVPLLSKYDDIHAICS 420
QY 421 LKDFLRLNKEPLTLFRLNRAFEAAEITDEDNSIAAMYQAVGELPQANRDTLAFMLIHL 480

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Db 421 LKDFLRNKEPLLFRLNRAFMFAEITDEDNISIAAMYQAVGELPQANRDTLAFIMIH 480
Qy 481 QRYAOSPHTRKMDVANLAKVFGPTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
Db 481 QRYAOSPHTRKMDVANLAKVFGPTIVAAVNPDPVTMLDIDKQPKVERLLSLPLEYWS 540
Qy 541 QPMWVQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQRYWS 600
Db 541 QPMWVQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQRYWS 600
Qy 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMLK 632
Db 601 TLTKNTPRFGSKSKSATNLGROGNFPASPMLK 632

RESULT 3
Q9NMN2 PRELIMINARY; PRT; 632 AA.
ID Q9NMN2;
AC Q9NMN2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ20726.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Odayashi M.,
RA Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isoqai T., Sugano S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000733; BAA91347.1; -.
DR HSP; Q98935; 1F7C.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR002219; DAG_P8-Bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; Cl.1; 1.
DR Pfam; PF00620; RhoGAP.1.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR SMART; SM00109; Cl.1.
DR SMART; SM00324; RhoGAP.1.
DR PROSITE; PS00479; DAG_P8_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_P8_BIND_DOM_2; 1.
DR PROSITE; PS00238; RHO_GAP.1.
SQ SEQUENCE 632 AA; 71048 MW; 7DC06CB725BBA44 CRC64;

Query Match
Best Local Similarity 99.7%; Score 3230; DB 2; Length 632;
Matches 630; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDTMNLVNLFEQVLRVVEILSEGNEVOFIQALQPEDFRKKMORTDHELKTKYKLLMK 60
Db 1 MDTMNLVNLFEQVLRVVEILSEGNEVOFIQALQPEDFRKKMORTDHELKTKYKLLMK 60
Qy 61 AETERSALVULKHANOVDAVEKRRORAEADCKERQQLIREMLMCDTSSISLSE 120
Db 61 AETERSALVULKHANOVDAVEKRRORAEADCKERQQLIREMLMCDTSSISLSE 120
Qy 121 QKSALAFNLRGQSSSSNAGKRLSTIDSGSILSDISFQTDSESLDMSISLVTFKLKTR 180
Db 121 QKSALAFNLRGQSSSSNAGKRLSTIDSGSILSHSIFQTDSESLDMSISLVTFKLKTR 180
Qy 181 EKRRSTSRQFVDPGPVKKTRSIGSAVDQNEISYAKTTVTVPNDGPIEAVSTETVP 240
Db 181 EKRRSTSRQFVDPGPVKKTRSIGSAVDQNEISYAKTTVTVPNDGPIEAVSTETVP 240

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Qy 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTEDSVGTPOSGMRLHDFVSKTVIRESC 300
Db 241 YWTRSRKKTGTLQPMNSDSTLNSRQLEPRTEDSVGTPOSGMRLHDFVSKTVIRESC 300
Qy 301 VPCGRKIKRGKSLKCRDRVVSHPKCRDPCPCPTLIGPVKIGEGMLADFVSQTSR 360
Db 301 VPCGRKIKRGKSLKCRDRVVSHPKCRDPCPCPTLIGPVKIGEGMLADFVSQTSR 360
Qy 361 MPSIVHCVNEIEQGLTETGLYRISGDRYVKEKEKFLKRYVPLSKYDDIAICS 420
Db 361 MPSIVHCVNEIEQGLTETGLYRISGDRYVKEKEKFLKRYVPLSKYDDIAICS 420
Qy 421 LKDFLRNKEPLLFRLNRAFMFAEITDEDNISIAAMYQAVGELPQANRDTLAFIMIH 480
Db 421 LKDFLRNKEPLLFRLNRAFMFAEITDEDNISIAAMYQAVGELPQANRDTLAFIMIH 480
Qy 481 QRYAOSPHTRKMDVANLAKVFGPTIVAAVNPDPVTMSODIKRQPKVERLLSLPLEYWS 540
Db 481 QRYAOSPHTRKMDVANLAKVFGPTIVAAVNPDPVTMLDIDKQPKVERLLSLPLEYWS 540
Qy 541 QPMWVQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQRYWS 600
Db 541 QPMWVQENIDPLHVIENSNAFSTPOTPDIKVSLGCVTTPEHQLKTPSSSSLSQRYWS 600

RESULT 4
Q9P250 PRELIMINARY; PRT; 570 AA.
ID Q9P250;
AC Q9P250;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA1478 protein (Fragment).
GN Name=KIAA1478;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:143-150 (2000).
DR EMBL; AB040911; BAA96002.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR002219; DAG_P8-Bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; Cl.1; 1.
DR Pfam; PF00620; RhoGAP.1.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR SMART; SM00109; Cl.1.
DR SMART; SM00324; RhoGAP.1.
DR PROSITE; PS00479; DAG_P8_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_P8_BIND_DOM_2; 1.
DR PROSITE; PS00238; RHO_GAP.1.
FT NON TER 1
SQ SEQUENCE 570 AA; 63468 MW; A03F36C0AA65485 CRC64;

Query Match
Best Local Similarity 90.0%; Score 2919; DB 2; Length 570;
Matches 569; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

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Matches 569, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 63 TERSALDVKLKHARNQVDVEIKRROAREADCEKLEROIOLIREMLMCDTSGSIOLSEBK 122
 DB 1 TERSALDVKLKHARNQVDVEIKRROAREADCEKLEROIOLIREMLMCDTSGSIOLSEBK 60
 QY 123 SALAFINRQOPSSSNAAGNKRSLSTIDBSGSIISDIFDKTDESILDMDSLVKTFKLKRRK 182
 DB 61 SALAFINRQOPSSSNAAGNKRSLSTIDBSGSIISDIFDKTDESILDMDSLVKTFKLKRRK 120
 QY 183 RRSRSTROPFDGPPGPKYKTRSIGSAVDQGNESIIVAKTTVTPVDGPIEAVSTIETVPW 242
 DB 121 RRSRSTROPFDGPPGPKYKTRSIGSAVDQGNESIIVAKTTVTPVDGPIEAVSTIETVPW 180
 QY 243 TRSRRKTGTLQPMNSDSTLNSROLBERTETDSVGTPOSGNGLHDFVSKTVIKPESQVP 302
 DB 181 TRSRRKTGTLQPMNSDSTLNSROLBERTETDSVGTPOSGNGLHDFVSKTVIKPESQVP 240
 QY 303 CGKRIKFGKLSLKCRDQVSVSHPECRDRCPLPCIPPLIGTPVKIGGMLADFVSQTSPI 362
 DB 241 CGKRIKFGKLSLKCRDQVSVSHPECRDRCPLPCIPPLIGTPVKIGGMLADFVSQTSPI 300
 QY 363 PSIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHAICSL 422
 DB 301 PSIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHAICSL 360
 QY 423 KDFLNLIKPEPLTFPLNRAFMEEAETIDEDNSIAAMYQAVGELPOANRDTLAFMIHLOR 482
 DB 361 KDFLNLIKPEPLTFPLNRAFMEEAETIDEDNSIAAMYQAVGELPOANRDTLAFMIHLOR 420
 QY 483 VAQSPHTKMDVANLAKVFEGPTIVAAHVPNDPVTMSODIKROPKVERLLSLPLEYWSQF 542
 DB 421 VAQSPHTKMDVANLAKVFEGPTIVAAHVPNDPVTMLQDIKROPKVERLLSLPLEYWSQF 480
 QY 543 MNVBEQENIDPLAVIENSNAFSTPQTPDIXSLGPTTPEHQLKTPSSSSLSQVRSL 602
 DB 481 MNVBEQENIDPLAVIENSNAFSTPQTPDIXSLGPTTPEHQLKTPSSSSLSQVRSL 540
 QY 603 TKNTPRFGSKSATNLGRQGNFFASPMUK 632
 DB 541 TKNTPRFGSKSATNLGRQGNFFASPMUK 570

RESULT 5

Q9BZ74 PRELIMINARY; PRT; 628 AA.

AC Q9BZ74; 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE FKSG42.
 GN Name=FKSG42; (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1] _SEQUENCE FROM N.A.
 RA Wang Y.-G., Gong L.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF34184; AAG50293.1; -;
 DR HSSP; Q98935; 1F7C.
 DR InterPro; IPR000198; RhogAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF00620; RhogAP; 1.
 DR SMART; SM00324; RhogAP; 1.
 DR PROSITE; PS50238; RHOGAP; 1.
 SQ SEQUENCE 628 AA; 70013 MW; A142855A613154CC CRC64;

Query Match 85.8%; Score 2781; DB 2; Length 628;
 Best Local Similarity 87.0%; Pred. No. 4,6e-164;
 Matches 550; Conservative 31; Mismatches 47; Indels 4; Gaps 2;

QY 1 MDTMLNLRNLFEOULVRVELISEGENVOFTOLADPEDFPKKORTDHELAKYKDLMK 60
 DB 1 MDTMLNLRNLFEOULVRGAEILKEGNELOFTOLVDFDFPKKMERITYELGKYDILK 60
 QY 61 ATERSALDVKLKHARNQVDVEIKRROAREADCEKLEROIOLIREMLMCDTSGSIOLSEBK 120
 DB 61 ATERSALDVKLKHARNQVDVEIKRROAREADCEKLEROIOLIREMLMCDTSGSIOLSEBK 120
 QY 121 OKSALAFINRQOPSSSNAAGNKRSLSTIDBSGSIISDIFDKTDESILDMDSLVKTFKLKRR 180
 DB 121 OKSALAFINRQOPSSSNAAGNKRSLSTIDBSGSIISDIFDKTDESILDMDSLVKTFKLKRR 180
 QY 181 EKRSTROPFDGPPGPKYKTRSIGSAVDQGNESIIVAKTTVTPVDGPIEAVSTIETVPW 240
 DB 181 EKRSTROPFDGPPGPKYKTRSIGSAVDQGNESIIVAKTTVTPVDGPIEAVSTIETVPW 240
 QY 241 YTRSRRKTGTLQPMNSDSTLNSROLBERTETDSVGTPOSGNGLHDFVSKTVIKPESQVP 300
 DB 241 YTRSRRKTGTLQPMNSDSTLNSROLBERTETDSVGTPOSGNGLHDFVSKTVIKPESQVP 300
 QY 301 VPCGRIRKFGKLSLKCRDQVSVSHPECRDRCPLPCIPPLIGTPVKIGGMLADFVSQTSPI 360
 DB 301 VPCGRIRKFGKLSLKCRDQVSVSHPECRDRCPLPCIPPLIGTPVKIGGMLADFVSQTSPI 360
 QY 361 MIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHAICSL 420
 DB 361 MIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKEIKKFLRVKTVPLSKVDIHAICSL 419
 QY 421 LKDFLNLIKPEPLTFPLNRAFMEEAETIDEDNSIAAMYQAVGELPOANRDTLAFMIHLOR 480
 DB 420 LKDFLNLIKPEPLTFPLNRAFMEEAETIDEDNSIAAMYQAVGELPOANRDTLAFMIHLOR 479
 QY 481 QVAPSPHTKMDVANLAKVFEGPTIVAAHVPNDPVTMSODIKROPKVERLLSLPLEYWS 540
 DB 480 QVAPSPHTKMDVANLAKVFEGPTIVAAHVPNDPVTMLQDIKROPKVERLLSLPLEYWS 539
 QY 541 QPMVBEQENIDPLAVIENSNAFSTPQTPDIXSLGPTTPEHQLKTPSSSSLSQVRSL 600
 DB 540 QPMVBEQENIDPLAVIENSNAFSTPQTPDIXSLGPTTPEHQLKTPSSSSLSQVRSL 596
 QY 601 TLTNTPRFGSKSATNLGRQGNFFASPMUK 632
 DB 597 TLTNTPRFGSKSATNLGRQGNFFASPMUK 628

RESULT 6

Q9WVW1 PRELIMINARY; PRT; 628 AA.

AC Q9WVW1; 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Rac_GTPase-activating protein (MgcracGAP variant alpha) (MgcracGAP
 GN Name=Racgap1; Synonyms=MgcracGAP;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_Taxid=10090;
 RN [1] _SEQUENCE FROM N.A.
 RA MEDLINE=99249188; PubMed=10235109;
 RA Woolferton E.J., Halotis T., Mueller C.R.;
 RT "Identification and characterization of a transcript for a novel Rac
 RT GTPase-activating protein in terminally differentiating 3T3-L1
 RT adipocytes.";
 RL DNA Cell Biol. 18:265-273(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435340; PubMed=10979956;
 RA Kawashima T., Hirose K., Satoh T., Kaneko A., Ikeda Y., Kaziro Y.,
 RA Nosaka T., Kitamura T.;
 RT "MgcracGAP is involved in the control of growth and differentiation of

RT hematopoietic cells." ;
 RL Blood 96:2116-2124(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1;
 RX MEDLINE=21184103; PubMed=11287179;
 RA Van de Putte T., Zwijnen A., Lonnay O., Rybin V., Cozijnsen M.,
 RA Francis A., Baekelandt V., Kozak C.A., Zerial M., Huybreckx D.,
 RT "Mice with a homozygous gene trap vector insertion in mrgacp die
 during pre-implantation development." ;
 RL Mech. Dev. 102:33-44(2001).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzyvinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maizra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF079974; AAD40487.1; -;
 DR EMBL; AB030252; BAA90248.1; -;
 DR EMBL; AF212320; AAG43539.1; -;
 DR EMBL; AF212321; AAG43540.1; -;
 DR EMBL; BC010715; AAI10715.1; -;
 DR HSSP; Q89935; 1F7C;
 DR MGD; MG1:1349423; Raccap1.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR001450; 4FeS_ferredoxin.
 DR InterPro; IPR002219; DAG_PE_bind.
 DR InterPro; IPR000198; RhoGAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF00130; Cl.1; 1.
 DR Pfam; PF00620; RhoGAP.1.
 DR PRINTS; PRO0353; 4FE4SFRDOXIN.
 DR SMART; SM00109; Cl.1.
 DR SMART; SM00324; RhoGAP.1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50238; RHO_GAP_1.
 DR SEQUENCE 628 AA; 70158 MW; 8D1B9DEC3CE057BE CRC64;
 QY Query Match 84.3%; Score 2734; DB 2; Length 628;
 Best Local Similarity 84.4%; Pred. No. 3.8e-161;
 Matches 534; Conservative 47; Mismatches 46; Indels 6; Gaps 3;
 QY 1 MDPMMLNVRLLFQOLVRVITLSEGN-VQFIQLADFPFRKKMOTDELKQYDLM 59
 DB 1 MDPMMLNVRLLFQOLVRVITLSEGN-VQFIQLADFPFRKKMOTDELKQYDLM 60

QY 60 KAETRSALDVKXKARNVDVEIKRQREADCEKLEQIQIIREMLMCTSGSIQLSE 119
 DB 61 KAETRSALDVKXKARNVDVEIKRQREADCEKLEQIQIIREMLMCTSGSIQLSE 120
 QY 120 EOKSALAFNLRGPPSSNMGRRLSTIDSGSLISDIPKQDESDMSLKTFTLK 179
 DB 121 EOKSALAFNLRGPPSSNMGRRLSTIDSGSLISDIPKQDESDMSLKTFTLK 180
 QY 180 REKRSTSRQFVGPFGPVYKTRTSIGSAVDQNESIVAKTVVVPNDGPIEAVSTIEY 239
 DB 181 REKRSTSRQFVGPFGPVYKTRTSIGSAVDQNESIVAKTVVVPNDGPIEAVSTIEY 240
 QY 240 PYWTSRRKRTGLQPNNSDSTLNSQLERPTETDVTGQNSGMLHDFSVKTVIKES 239
 DB 241 PYWTSRRKRTGLQPNNSDSTLNSQLERPTETDVTGQNSGMLHDFSVKTVIKES 300
 QY 300 CVPCGRIRKFKSLKSCRCRVVSHRECDRCPLPCLITLIGTPVYIGEMLADFPVSQTS 359
 DB 301 CVPCGRIRKFKSLKSCRCRVVSHRECDRCPLPCLITLIGTPVYIGEMLADFPVSQTS 360
 QY 360 PMIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKELKEKFLKVTVPPLSKYDDIHAIC 419
 DB 361 PMIPSIIVHCVNEIEORGLTETGLYRISGCDRTVKELKEKFLKVTVPPLSKYDDIHAIC 420
 QY 420 SLKDEFLRLKEPLTFRINRAFEAEITDEDSIAAMYQAVGELPQANRDTLAFIMH 479
 DB 421 SLKDEFLRLKEPLTFRINRAFEAEITDEDSIAAMYQAVGELPQANRDTLAFIMH 480
 QY 480 LQVVAOSPHTKMDVNLAKVFGPTIYAAVNPDPPTMSODIRGQKRVVERLLSLPLEYV 539
 DB 481 LQVVAOSPHTKMDVNLAKVFGPTIYAAVNPDPPTMSODIRGQKRVVERLLSLPLEYV 540
 QY 540 SCFMVTEOENIDPLAVIENSNAFSTPOTPDIKSLGPTVTPPHOILKTPSSSLSORVR 599
 DB 541 SCFMVTEOENIDPLAVIENSNAFSTPOTPDIKSLGPTVTPPHOILKTPSSSLSORVR 596
 QY 600 STLTNTPRFGSKSKSATNLGRQGNFASPMK 632
 DB 597 N-LSKSTPRGNKSKSATNLGGQKFPAPYLK 628
 RESULT 7
 ID 06NRH9 PRELIMINARY; PRT; 629 AA.
 AC 06NRH9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE MGC83804 (TREMBlrel. 27, Last annotation update)
 GN Name=MGC83804;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocytes;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
RT Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC070771; AAH70771.1; -.
DR InterPro: IPR001450; 4Fe4S ferredoxin.
DR InterPro: IPR002219; DAG PE-bind.
DR InterPro: IPR001198; RhOGAP.
DR InterPro: IPR008936; Rho_GAP.
DR Pfam: PF00130; Cl_1; 1.
DR Pfam: PF00620; RhOGAP; 1.
DR PRINTS: PR00353; 4Fe4SFRDOXIN.
DR SMART: SM00109; Cl_1.
DR SMART: SM00324; RhOGAP; 1.
DR PROSITE: PS00479; DAG PE BIND DOM 1; 1.
DR PROSITE: PS50081; DAG PE BIND DOM 2; 1.
DR PROSITE: PS50238; RhOGAP; 1.
SQ SEQUENCE 629 AA; 70781 MW; 40BB97C1CEADFC2 CRC64;

Query Match 77.0%; Score 2497.5; DB 2; Length 629;
Best Local Similarity 76.1%; Pred. No. 1.8e-146;
Matches 482; Conservative 78; Mismatches 68; Indels 5; Gaps 4;

1 MDTMMLNVLNLFEOALVRREILSEGENVOFIOLADFEFRKKMQRTHDELKYLKDLMLK 60
1 MATNMLNVLNLFEOALVRREILSEGENVOFIOLADFEFRKKMQRTHDELKYLKDLMLK 60
61 AETESALDVKLKAHQVDAVEIKRQRAEADCEKLEROIQIREMLMCDTSGSIOLESB 120
61 TETESALDVKLKAHQVDAVEIKRQRAEADCEKLEROIQIREMLMCDTSGSIOLESB 120
121 QKSALAFL-NRQOPSSNAGNKLSTLIDSSGSLISLISFDKTDSDSLDMSSLYKTFKLK 179
121 QKSALAFLNRTQMSADNGTRRLSTLIDSSGSLISLISFDKTDSDSLDMSSLYKTFKLK 180
180 REKRSTSRQFVDPGPPVFKTRISIGSAVDQGNESIVAKTVTVPRDGGPIEAVSTIEV 239
181 REKRSTSRQFVDPGPPVFKTRISIGSAVDQGNESIVAKTVTVPRDGGPIEAVSTIEV 239
240 PYWTRSRRTKGTGLQPNWSDSTLNSRQLEPRTEISVGTIPQSGNGLMDFVSKTVIKPS 299
240 PYWTRSRRTKGTGLQPNWSDSTLNSRQLEPRTEISVGTIPQSGNGLMDFVSKTVIKPS 299
240 PYWTRSRRTKGTGLQPNWSDSTLNSRQLEPRTEISVGTIPQSGNGLMDFVSKTVIKPS 298
300 CYPCKGRIRFGLSLKCRDRCRVASHCEGDRCPPLPILIGTPVKIKGMLADPFSQTS 359
300 CYPCKGRIRFGLSLKCRDRCRVASHCEGDRCPPLPILIGTPVKIKGMLADPFSQTS 359
299 CYPCKGRIRFGLSLKCRDRCRVASHCEGDRCPPLPILIGTPVKIKGMLADPFSQTS 358
360 PMIPSTIVACNIEIQRGLTETGLVIRISGCDRTVKEKLEKFLRVKVPPLSKVDIHAIC 419
360 PMIPSTIVACNIEIQRGLTETGLVIRISGCDRTVKEKLEKFLRVKVPPLSKVDIHAIC 419
359 PMIPSTIVACNIEIQRGLTETGLVIRISGCDRTVKEKLEKFLRVKVPPLSKVDIHAIC 418
420 SLTKDFLRNLKEPLLTFRNLRAFMEEAETIDEDNSIAAMYQAVGELPQANRDTLAFMTM 479
420 SLTKDFLRNLKEPLLTFRNLRAFMEEAETIDEDNSIAAMYQAVGELPQANRDTLAFMTM 479
419 GLTKDFLRNLKEPLLTFRNLRAFMEEAETIDEDNSIAAMYQAVGELPQANRDTLAFMTM 478
480 LORVQASPTKMDVANLAVFGFTIYAAAVPNDDPYTMSQDIKQPKVVERLISLPLEY 539
480 LORVQASPTKMDVANLAVFGFTIYAAAVPNDDPYTMSQDIKQPKVVERLISLPLEY 539
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DB 479 LORVQASPTKMDVANLAVFGFTIYAAAVPNDDPYTMSQDIKQPKVVERLISLPLEY 538
QY 540 SQPMVVEQENIDPLHVIENSNAFSTPQPDIKVSLGPAVTPPEHQLKTPSSSSSQRVR 599
DB 539 NQYMYV--ENIDPNHIIENSNVFSTPQPDPAVSLGPAVTPPEHQLKTPSSSSSQRVK 596
QY 600 STLTKNTPRFSGSKSATNLGROGNFASPMUK 632
DB 597 STLSKNTPFSGSKSATNLGROGNFASPMUK 629

RESULT 8
AAH70771 PRELIMINARY; PRT; 629 AA.
AC AAH70771;
DT 13-MAY-2004 (TREMBlrel. 27, Created)
DT 13-MAY-2004 (TREMBlrel. 27, Last sequence update)
DT 13-MAY-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCB|TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
RT Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC070771; AAH70771.1; -.
KW Hypothetical protein.
SQ SEQUENCE 629 AA; 70781 MW; 40BB97C1CEADFC2 CRC64;

Query Match 77.0%; Score 2497.5; DB 2; Length 629;
Best Local Similarity 76.1%; Pred. No. 1.8e-146;
Matches 482; Conservative 78; Mismatches 68; Indels 5; Gaps 4;

1 MDTMMLNVLNLFEOALVRREILSEGENVOFIOLADFEFRKKMQRTHDELKYLKDLMLK 60
1 MATNMLNVLNLFEOALVRREILSEGENVOFIOLADFEFRKKMQRTHDELKYLKDLMLK 60
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QY 61 ATERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQILIRELMCDTSGSIQLSSE 120
 DB 61 TERSALREVLKHAHQVDEIKRQRAEADCEKLEROIQILIRELMCDPSSGSIQLSSE 120
 QY 121 QRSALAFI-NRQOPSSNAGKRLSTIDSSGSLSDISPDKTESIDMSSLYKTRK 179
 DB 121 QRSALAFI-NRQOPSSNAGKRLSTIDSSGSLSDISPDKTESIDMSSLYKTRK 180
 QY 180 REKRSTSRQFVDPGPPVKTSTIGSAVDQNESIVAKTIVTVPDNGPIEAVSTIET 239
 DB 181 REKRSTSRQFVDPGPPVKTSTIGSAVDQNESIVAKTIVTVPDNGPIEAVSTIET 239
 QY 240 PYWTSRRRTGTGLQPNNSDSTINSRLQLEPRTETDSVGTPOSGKMLHDFVSKTVIKPSS 299
 DB 240 PYWTSRRRTGTGLQPNNSDSTINSRLQLEPRTETDSVGTPOSGKMLHDFVSKTVIKPSS 298
 QY 300 CVPCKGRIFGKLSLKCRDQVSVHPECRCPLPCTIPLTIGTPVKIGGMLADPVSQTS 359
 DB 299 CVPCKGRIFGKLSLKCRDQVSVHPECRCPLPCTIPLTIGTPVKIGGMLADPVSQTS 358
 QY 360 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKFLRVKTVPLISKVDIHAIC 419
 DB 359 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKFLRVKTVPLISKVDIHAIC 418
 QY 420 SLIKDFLRMLKEPLLTFRINRAFMEEAETDEDNSTIANYQAVGELPOANRDTLAFIMH 479
 DB 419 GFLKDFLRMLKEPLLTFRINRAFMEEAETDEDNSTIANYQAVGELPOANRDTLAFIMH 478
 QY 480 LORVVASPHTKQDVANLAVFPGTIVAAVNPDPVYTSODIKRQPKVVERLISLPLEY 539
 DB 479 LORVVASPHTKQDVANLAVFPGTIVAAVNPDPVYTSODIKRQPKVVERLISLPLEY 538
 QY 540 SQPMWEGENIDPLVHENSNAFSTPOTDIXSLIGPVTPEHOLKTPSSSSLSORR 599
 DB 539 SQPMWEGENIDPLVHENSNAFSTPOTDIXSLIGPVTPEHOLKTPSSSSLSORR 596
 QY 600 STLTNTTPRFGSKSKSATNLGROGNFASPMLK 632
 DB 597 STLTNTTPRFGSKSKSATNLGROGNFASPMLK 629

RESULT 9
 Q6NVLL PRELIMINARY; PRT; 629 AA.
 AC Q6NVLL: 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein MGC69444.
 GN Name=MGC69444;
 OS Xenopus tropicalis (western clawed frog) (Silurana¹ tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBI_Taxid=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marcus M.B., Farmer A.A., Rubin G.M., Hong L.,
 Stalcup M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueidi T.B., Tohyuki S., Carninci P., Prange C.,
 Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
 RA Kravynetski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RA EMBL: BC067994; AA067994.1; -
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR002219; DAG_PE_bind.
 DR InterPro: IPR000198; RhoGAP.
 DR InterPro: IPR008936; Rho_GAP.
 DR Pfam: PF00130; C1_1; 1.
 DR Pfam: PF0620; RhoGAP; 1.
 DR PRINTS: PR00353; 4FE4SFRDOXIN.
 DR SMART: SM00109; C1; 1.
 DR SMART: SM00324; RhoGAP; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS00681; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS50238; RHO_GAP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 629 AA; 7111 MW; BF17EBBA3456077A CRC64;

Query Match 76.4%; Score 2476.5; DB 2; Length 629;
 Best Local Similarity 75.5%; Pred. No. 3.6e-145;
 Matches 478; Conservative 77; Mismatches 73; Indels 5; Gaps 4;

QY 1 MPTMNLVNLPEOLVRARVEISSENEVOFIQADPEFRKKWORTDEHLYKQDLMK 60
 DB 1 MATMNLNLNLEBOLKRVQDGLNEGLEPOFIQAKNFEDFRKKWQSEBOLIKKMKLMK 60
 QY 61 ATERSALDVLKHAHQVDEIKRQRAEADCEKLEROIQILIRELMCDTSGSIQLSSE 120
 DB 61 TERSALREVLKHAHQVDEIKRQRAEADCEKLEROIQILIRELMCDPSSGSIQLSSE 120
 QY 121 QRSALAFI-NRQOPSSNAGKRLSTIDSSGSLSDISPDKTESIDMSSLYKTRK 179
 DB 121 QRSALAFI-NRQOPSSNAGKRLSTIDSSGSLSDISPDKTESIDMSSLYKTRK 180
 QY 180 REKRSTSRQFVDPGPPVKTSTIGSAVDQNESIVAKTIVTVPDNGPIEAVSTIET 239
 DB 181 REKRSTSRQFVDPGPPVKTSTIGSAVDQNESIVAKTIVTVPDNGPIEAVSTIET 239
 QY 240 PYWTSRRRTGTGLQPNNSDSTINSRLQLEPRTETDSVGTPOSGKMLHDFVSKTVIKPSS 299
 DB 240 PYWTSRRRTGTGLQPNNSDSTINSRLQLEPRTETDSVGTPOSGKMLHDFVSKTVIKPSS 298
 QY 300 CVPCKGRIFGKLSLKCRDQVSVHPECRCPLPCTIPLTIGTPVKIGGMLADPVSQTS 359
 DB 299 CVPCKGRIFGKLSLKCRDQVSVHPECRCPLPCTIPLTIGTPVKIGGMLADPVSQTS 358
 QY 360 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKFLRVKTVPLISKVDIHAIC 419
 DB 359 PIMPSTIVHCNEIEBQGLTETGLYRISGCDRTVKEIKKFLRVKTVPLISKVDIHAIC 418
 QY 420 SLIKDFLRMLKEPLLTFRINRAFMEEAETDEDNSTIANYQAVGELPOANRDTLAFIMH 479
 DB 419 GFLKDFLRMLKEPLLTFRINRAFMEEAETDEDNSTIANYQAVGELPOANRDTLAFIMH 478
 QY 480 LORVVASPHTKQDVANLAVFPGTIVAAVNPDPVYTSODIKRQPKVVERLISLPLEY 539
 DB 479 LORVVASPHTKQDVANLAVFPGTIVAAVNPDPVYTSODIKRQPKVVERLISLPLEY 538
 QY 540 SQPMWEGENIDPLVHENSNAFSTPOTDIXSLIGPVTPEHOLKTPSSSSLSORR 599
 DB 539 SQPMWEGENIDPLVHENSNAFSTPOTDIXSLIGPVTPEHOLKTPSSSSLSORR 596
 QY 600 STLTNTTPRFGSKSKSATNLGROGNFASPMLK 632

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DB 597 STIGKNTMFGSKSKSVSSIPROGNFASPMLK 629
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RESULT 10
AAH67994 PRELIMINARY; PRT; 629 AA.
AC AAH67994;
DT 01-JUN-2004 (TRENBLrel. 27, Created)
DT 01-JUN-2004 (TRENBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TRENBLrel. 27, Last annotation update)
DE MGC69444 protein.
GN MGC69444
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC067994, AAH67994.1, -.
SQ SEQUENCE 629 AA; 7111 MW; BF17EB8A3456077A CRC64;

Query Match 76.4%; Score 2476.5; DB 2; Length 629;
Best Local Similarity 75.5%; Pred. No. 3.6e-145;
Matches 478; Conservative 77; Mismatches 73; Indels 5; Gaps 4;

QY 1 MDTMLNENFQOLVRYEIISENEVOFIQIAKDFEDFRKKQRTDHELKYLK 60
DB 1 MATNLMNENFQOLVRYEIISENEVOFIQIAKDFEDFRKKQRTDHELKYLK 60
QY 61 AATERSALDUKXKHAHQVDEIKKQRAEADCEKLEKROITOLIRELMCDTSSISLSE 120
DB 61 TETESALEVKKLKHANQVDEIKKQRAEADCEKLEKROITOLIRELMCDTSSISLSE 120
QY 121 OKSALAFU-NGOPSSNAGNKRLLSTIDSGSLISDPDKTDESIDMDSLVKTKFLK 179
DB 121 QRSALAFU-NGOPSSNAGNKRLLSTIDSGSLISDPDKTDESIDMDSLVKTKFLK 180
QY 180 REKRSTSRQFVDPGPVYKTRTSGSAVDQNESIVAKTVTVVNDGQPIEAVSTIEV 239
DB 181 REKRSTSRQFVDPGPVYKTRTSGSAVDQNESIVAKTVTVVNDGQPIEAVSTIEV 239
QY 240 PYWTSSRKCTGTLOPNSDSTLNSRQLETRTETDSVGTQSGNGKRLHDFVSKTVIKPS 299
DB 240 PYWTSSRKCTGTLOPNSDSTLNSRQLETRTETDSVGTQSGNGKRLHDFVSKTVIKPS 299
DB 240 PYWTSSRKCTGTLOPNSDSTLNSRQLETRTETDSVGTQSGNGKRLHDFVSKTVIKPS 298
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QY 300 CYPCKGRKIKFGKLSIAKCRDVRVSHPEGRDRCPILPILIGTPYKIGKMLADPVSQTS 359
DB 299 CYPCKGRKIKFGKLSIAKCRDVRVSHPEGRDRCPILPILIGTPYKIGKMLADPVSQTS 358
QY 360 PMIPSIWVCVNEIORGLTETGLYRISGCDRTVELKEKFRVKTVPILYSKYDIIHAIC 419
DB 359 PMIPPIVHCVSEIORGLHETGLYRISGCDRTVELKEKFRGKSVPLISKYDIIHANC 418
QY 420 SILKDFLRNKEPLLTFRINRAFMBAEITBDSIAAMYQAVGEIPOANDTLAFLMT 479
DB 419 GFLKDFLRNKEPLLTFRINRAFMBAEITBDSIAAMYQAVGEIPOANDTLAFLMT 478
QY 480 LORVQSPHTKDVANLAKVFGEPTTVAHNAVPPDVTMSQDIKROPKYVERILSLPLEW 539
DB 479 LORVQSPHTKDVANLAKVFGEPTTVAHNAVPPDVTMSQDIKROPKYVERILSLPLEW 538
QY 540 SOFMVVEQENIDELFVITENSNAFSTPQIPDILVSLGPTTPEHOLLTPSSSSISQRYR 599
DB 539 NOFMVVE-ENIDFNHITENAVNFTPTPDARVSMGLPTTPEQOPNKTPSSSSISQRYR 596
QY 600 STLTGNTMFGSKSKSATNLGROGNFASPMLK 632
DB 597 STIGKNTMFGSKSKSVSSIPROGNFASPMLK 629
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RESULT 11
Q7ZWM6 PRELIMINARY; PRT; 629 AA.
ID Q7ZWM6;
AC Q7ZWM6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2004 (TRENBLrel. 26, Last annotation update)
DE MGC53048 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genomic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
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Db 121 EORSALAFINARSONPANINTSRRLATIDESASIIISDYSYKTDSDLDWSSAIRTRIX 180
Qy 179 KREKRRSTSRQFVDPGPPGVKTRSIGSAVDQGNESIVAKTTVTVPNDGPIEAVSTIET 238
Db 181 KRQKRS-SRNTTEGPAAKRSRSTGRSEKGNESIVAKTTVTVPADGGPIEAVTVVA 239
Qy 239 VPYWTRSRRT-----GTLOPNMSDSLNSROLE-----PRTEDS-VG 276
Db 240 VPYWTRSRRTVFCSESECISINYSAAVEMDTVDTSVQSMDFKQPSLPNAENRAPS 299
Qy 277 TPQSGKRLHDFVSCVTIVKPPESCVRPGKRIKFKGLSLKCRDVRVSHPECRDRCPLCI 336
Db 300 TPQSGKRLHDFVSCVTIVKPPESCVRPGKRIKFKGLSLKCRDVRVSHPECRDRCPLCI 359
Qy 337 PTLIGTPVKIGBMLADPVFSQTSMPMPSIVHCVNEIEQRLTEGLYRISGCDRTVKEL 396
Db 360 PSMGTGPVKIGBGLTANVSNTPMPSIVHCVNEIEQRLTEGLYRISGCDRTVKEL 419
Qy 397 KEKFLRVKTPVLLSKVDDIHAICSLIKDFLRNKEPILTFRLNRAFMFAETITDEDNIA 456
Db 420 KEKFLRVKTPVLLSKVDDIHAICSLIKDFLRNKEPILTFRLNRAFMFAETITDEDNIA 479
Qy 457 ANYQAVGELPOANRDTLAFIMHLOQVVAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVT 516
Db 480 LMVQNISDLPQPHRDTLAFILHLOQVVAOSPHTKMDITNLARVFGPTIVGHAVSNEPMT 539
Qy 517 MSQDIKROPKVERLLSLPLEYWSQPMVEQENIDPLH-VIENSNAFSTPQTDIVKSL 575
Db 540 IIQDTRKQPRVVERLLSLPLEYWSQPMIDHDHARDHMIINAVHT---TPDQMSMF 596
Qy 576 GCVTTPEHOLLTPSSSSLSQVR-STLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
Db 597 GVTTPDQMSKTPSSSSLSQRMKATLNAITPKFSSRSRAVAAVPRQGNFPASPMLK 654
RESULT 13
AAH63983 PRELIMINARY; PRT; 654 AA.
AC AAH63983;
DT 25-MAR-2004 (TReMBLrel. 27, Created)
DT 25-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein racgap1.
GN RACGAP1.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Musina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Kodrigues S., Sanchez A.,
RA Whiting M., Maan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."/;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC063983; AAH63983.1; -.
KW Hypothetical protein.
SQ SEQUENCE 654 AA; 73198 MW; CB656C1758B86DD8 CRC64;
Query Match 67.0%; Score 2173; DB 2; Length 654;
Best Local Similarity 64.6%; Pred. No. 2,5e-126;
Matches 425; Conservative 104; Mismatches 99; Indels 30; Gaps 9;
Qy 1 MDTMLANRNLFEQVLRVEIISGEVEVQIOLADQFEDFRKKQRTDHELCKYDLMK 60
Db 1 METAVMNIHSIFESIRADADVINESIEPQIOLAINFENRRMRRLBELNACKCEVLTK 60
Qy 61 AETRSALDVKLKHARNVDVIEIKRORAEADCEKLEQIOIIRLMQCD-TSGSIQISE 119
Db 61 AETRGALAEVKLKHARNVDVIEIRROKASECAKLDQILRELVSESSSIQIME 120
Qy 120 EORSALAFIN-RGQSSSNAGNKRSLTIDESGSIISDIFDKTDESLDWSSAIRTRIX 178
Db 121 EORSALAFINARSONPANINTSRRLATIDESASIIISDYSYKTDSDLDWSSAIRTRIX 180
Qy 179 KREKRRSTSRQFVDPGPPGVKTRSIGSAVDQGNESIVAKTTVTVPNDGPIEAVSTIET 238
Db 181 KRQKRS-SRNTTEGPAAKRSRSTGRSEKGNESIVAKTTVTVPADGGPIEAVTVVA 239
Qy 239 VPYWTRSRRT-----GTLOPNMSDSLNSROLE-----PRTEDS-VG 276
Db 240 VPYWTRSRRTVFCSESECISINYSAAVEMDTVDTSVQSMDFKQPSLPNAENRAPS 299
Qy 277 TPQSGKRLHDFVSCVTIVKPPESCVRPGKRIKFKGLSLKCRDVRVSHPECRDRCPLCI 336
Db 300 TPQSGKRLHDFVSCVTIVKPPESCVRPGKRIKFKGLSLKCRDVRVSHPECRDRCPLCI 359
Qy 337 PTLIGTPVKIGBMLADPVFSQTSMPMPSIVHCVNEIEQRLTEGLYRISGCDRTVKEL 396
Db 360 PSMGTGPVKIGBGLTANVSNTPMPSIVHCVNEIEQRLTEGLYRISGCDRTVKEL 419
Qy 397 KEKFLRVKTPVLLSKVDDIHAICSLIKDFLRNKEPILTFRLNRAFMFAETITDEDNIA 456
Db 420 KEKFLRVKTPVLLSKVDDIHAICSLIKDFLRNKEPILTFRLNRAFMFAETITDEDNIA 479
Qy 457 ANYQAVGELPOANRDTLAFIMHLOQVVAOSPHTKMDVANLAKVFGPTIVAAHVPNDPVT 516
Db 480 LMVQNISDLPQPHRDTLAFILHLOQVVAOSPHTKMDITNLARVFGPTIVGHAVSNEPMT 539
Qy 517 MSQDIKROPKVERLLSLPLEYWSQPMVEQENIDPLH-VIENSNAFSTPQTDIVKSL 575
Db 540 IIQDTRKQPRVVERLLSLPLEYWSQPMIDHDHARDHMIINAVHT---TPDQMSMF 596
Qy 576 GCVTTPEHOLLTPSSSSLSQVR-STLTNTPRFGSKSKSATNLGROGNFPASPMLK 632
Db 597 GVTTPDQMSKTPSSSSLSQRMKATLNAITPKFSSRSRAVAAVPRQGNFPASPMLK 654
RESULT 14
AAH63983 PRELIMINARY; PRT; 612 AA.
AC AAH63983;
DT 01-OCT-2004 (TReMBLrel. 28, Created)
DT 01-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.

Best Local Similarity	99.2%;	Pred. No. 2e-65;	
Matches 234;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	397	KEKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLTFRLNRAFMFAAEITDEDSIA	456
Db	20	KLKFLRVKTVPLLSKVDDIHAICSLKDFLRNLKEPLTFRLNRAFMFAAEITDEDSIA	79
QY	457	AMYQAVGELPQANRDTLAFMLHLOFVAQSPHTKMDVANLAKYFGPTIVAHAVPNDPVT	516
Db	80	AMYQAVGELPQANRDTLAFMLHLOFVAQSPHTKMDVANLAKYFGPTIVAHAVPNDPVT	139
QY	517	MSODIKROPKVVERLISLPLEYWSQFMVBOENIDPLHVIENSNAFSTPQTPDIXSLIG	576
Db	140	MLQDIKROPKVVERLISLPLEYWSQFMVBOENIDPLHVIENSNAFSTPQTPDIXSLIG	199
QY	577	PVTTPEHQLLKTSSSSSLSQRVSTLTNTPRFGSKSKSATNLGROGNFFASPMLK	632
Db	200	PVTTPEHQLLKTSSSSSLSQRVSTLTNTPRFGSKSKSATNLGROGNFFASPMLK	255

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